

## Sequence Table

## (2) INFORMATION FOR SEQ ID NO: 1:

## 5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

10 (iii) HYPOTHETICAL: No

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

15 (D) CLONE NAME: HP01263

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

20	Met	Gly	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Cys	Ile	Leu	Val	Leu	Cys	Cys
	1				5					10					15	
	Gly	Ala	Met	Ser	Pro	Pro	Gln	Leu	Ala	Leu	Asn	Pro	Ser	Ala	Leu	Leu
				20					25					30		
	Ser	Arg	Gly	Cys	Asn	Asp	Ser	Asp	Val	Leu	Ala	Val	Ala	Gly	Phe	Ala
			35					40					45			
25	Leu	Arg	Asp	Ile	Asn	Lys	Asp	Arg	Lys	Asp	Gly	Tyr	Val	Leu	Arg	Leu
		50					55				60					
	Asn	Arg	Val	Asn	Asp	Ala	Gln	Glu	Tyr	Arg	Arg	Gly	Gly	Leu	Gly	Ser
		65				70				75				80		
	Leu	Phe	Tyr	Leu	Thr	Leu	Asp	Val	Leu	Glu	Thr	Asp	Cys	His	Val	Leu
30				85					90					95		
	Arg	Lys	Lys	Ala	Trp	Gln	Asp	Cys	Gly	Met	Arg	Ile	Phe	Phe	Glu	Ser
			100					105					110			
	Val	Tyr	Gly	Gln	Cys	Lys	Ala	Ile	Phe	Tyr	Met	Asn	Asn	Pro	Ser	Arg
			115				120						125			
35	Val	Leu	Tyr	Leu	Ala	Ala	Tyr	Asn	Cys	Thr	Leu	Arg	Pro	Val	Ser	Lys
		130					135					140				
	Lys	Lys	Ile	Tyr	Met	Thr	Cys	Pro	Asp	Cys	Pro	Ser	Ser	Ile	Pro	Thr
	145					150				155				160		

	Asp	Ser	Ser	Asn	His	Gln	Val	Leu	Glu	Ala	Ala	Thr	Glu	Ser	Leu	Ala	
	Lys	Tyr	Asn	Asn	Glu	Asn	Thr	Ser	Lys	Gln	Tyr	Ser	Leu	Phe	Lys	Val	
5	Thr	Arg	Ala	Ser	Ser	Gln	Trp	Val	Val	Gly	Pro	Ser	Tyr	Phe	Val	Glu	
	Tyr	Leu	Ile	Lys	Glu	Ser	Pro	Cys	Thr	Lys	Ser	Gln	Ala	Ser	Ser	Cys	
	Ser	Leu	Gln	Ser	Ser	Asp	Ser	Val	Pro	Val	Gly	Leu	Cys	Lys	Gly	Ser	
10	225																240
	Leu	Thr	Arg	Thr	His	Trp	Glu	Lys	Phe	Val	Ser	Val	Thr	Cys	Asp	Phe	
	Phe	Glu	Ser	Gln	Ala	Pro	Ala	Thr	Gly	Ser	Glu	Asn	Ser	Ala	Val	Asn	
15	Gln	Lys	Pro	Thr	Asn	Leu	Pro	Lys	Val	Glu	Glu	Ser	Gln	Gln	Lys	Asn	
	Thr	Pro	Pro	Thr	Asp	Ser	Pro	Ser	Lys	Ala	Gly	Pro	Arg	Gly	Ser	Val	
	Gln	Tyr	Leu	Pro	Asp	Leu	Asp	Asp	Lys	Asn	Ser	Gln	Glu	Lys	Gly	Pro	
20	305																320
	Gln	Glu	Ala	Phe	Pro	Val	His	Leu	Asp	Leu	Thr	Thr	Asn	Pro	Gln	Gly	
	Glu	Thr	Leu	Asp	Ile	Ser	Phe	Leu	Phe	Leu	Glu	Pro	Met	Glu	Glu	Lys	
25	Leu	Val	Val	Leu	Pro	Phe	Pro	Lys	Glu	Lys	Ala	Arg	Thr	Ala	Glu	Cys	
	Pro	Gly	Pro	Ala	Gln	Asn	Ala	Ser	Pro	Leu	Val	Leu	Pro	Pro			

30

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317

(B) TYPE: Amino acid

35

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP01299

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

Met Trp Leu Tyr Leu Ala Ala Phe Val Gly Leu Tyr Tyr Leu Leu His
  1             5             10             15
10 Trp Tyr Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val
    20             25             30
Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln
    35             40             45
Leu Asp Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys
15     50             55             60
Gly Ala Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val
    65             70             75             80
Thr Leu Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp
    85             90             95
20 Val Lys Glu His Val Gly Asp Arg Gly Leu Trp Gly Leu Val Asn Asn
    100            105            110
Ala Gly Ile Leu Thr Pro Ile Thr Leu Cys Glu Trp Leu Asn Thr Glu
    115            120            125
Asp Ser Met Asn Met Leu Lys Val Asn Leu Ile Gly Val Ile Gln Val
25     130            135            140
Thr Leu Ser Met Leu Pro Leu Val Arg Arg Ala Arg Gly Arg Ile Val
    145            150            155            160
Asn Val Ser Ser Ile Leu Gly Arg Val Ala Phe Phe Val Gly Gly Tyr
    165            170            175
30 Cys Val Ser Lys Tyr Gly Val Glu Ala Phe Ser Asp Ile Leu Arg Arg
    180            185            190
Glu Ile Gln His Phe Gly Val Lys Ile Ser Ile Val Glu Pro Gly Tyr
    195            200            205
Phe Arg Thr Gly Met Thr Asn Met Thr Gln Ser Leu Glu Arg Met Lys
35     210            215            220
Gln Ser Trp Lys Glu Ala Pro Lys His Ile Lys Glu Thr Tyr Gly Gln
    225            230            235            240
Gln Tyr Phe Asp Ala Leu Tyr Asn Ile Met Lys Glu Gly Leu Leu Asn

```

245                      250                      255  
 Cys Ser Thr Asn Leu Asn Leu Val Thr Asp Cys Met Glu His Ala Leu  
                          260                      265                      270  
 Thr Ser Val His Pro Arg Thr Arg Tyr Ser Ala Gly Trp Asp Ala Lys  
 5                      275                      280                      285  
 Phe Phe Phe Ile Pro Leu Ser Tyr Leu Pro Thr Ser Leu Ala Asp Tyr  
                          290                      295                      300  
 Ile Leu Thr Arg Ser Trp Pro Lys Pro Ala Gln Ala Val  
 305                      310                      315

10

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

15                      (A) LENGTH: 296  
                          (B) TYPE: Amino acid  
                          (D) TOPOLOGY: Linear  
 (ii) SEQUENCE KIND: Protein  
 (iii) HYPOTHETICAL: No

20

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Liver  
 (D) CLONE NAME: HP01347

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Ser Asp Ser Lys Glu Pro Arg Val Gln Gln Leu Gly Leu Leu Gly  
   1                      5                      10                      15  
 Cys Leu Gly His Gly Ala Leu Val Leu Gln Leu Leu Ser Phe Met Leu  
 30                      20                      25                      30  
 Leu Ala Gly Val Leu Val Ala Ile Leu Val Gln Val Ser Lys Val Pro  
                          35                      40                      45  
 Ser Ser Leu Ser Gln Glu Gln Ser Glu Gln Asp Ala Ile Tyr Gln Asn  
                          50                      55                      60  
 35 Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys  
                          65                      70                      75                      80  
 Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly  
                          85                      90                      95

Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr  
                   100                  105                  110  
 Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln  
                   115                  120                  125  
 5 Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu  
                   130                  135                  140  
 Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu  
                   145                  150                  155                  160  
 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile  
 10                  165                  170                  175  
 Tyr Gln Glu Leu Thr Glu Leu Lys Ala Ala Val Gly Glu Leu Pro Glu  
                   180                  185                  190  
 Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala  
                   195                  200                  205  
 15 Ala Val Gly Glu Leu Pro Asp Gln Ser Lys Gln Gln Gln Ile Tyr Gln  
                   210                  215                  220  
 Glu Leu Thr Asp Leu Lys Thr Ala Phe Glu Arg Leu Cys Arg His Cys  
                   225                  230                  235                  240  
 Pro Lys Asp Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn  
 20                  245                  250                  255  
 Ser Gln Arg Asn Trp His Asp Ser Val Thr Ala Cys Gln Glu Val Arg  
                   260                  265                  270  
 Ala Gln Leu Val Val Ile Lys Thr Ala Glu Glu Gln Leu Pro Ala Val  
                   275                  280                  285  
 25 Leu Glu Gln Trp Arg Thr Gln Gln  
                   290                  295

## (2) INFORMATION FOR SEQ ID NO: 4:

## 30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

## 35 (iii) HYPOTHETICAL: No

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP01440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

5  
 Met Cys Thr Gly Lys Cys Ala Arg Cys Val Gly Leu Ser Leu Ile Thr  
     1                    5                    10                    15  
 Leu Cys Leu Val Cys Ile Val Ala Asn Ala Leu Leu Leu Val Pro Asn  
                     20                    25                    30  
 10 Gly Glu Thr Ser Trp Thr Asn Thr Asn His Leu Ser Leu Gln Val Trp  
                     35                    40                    45  
 Leu Met Gly Gly Phe Ile Gly Gly Gly Leu Met Val Leu Cys Pro Gly  
                     50                    55                    60  
 Ile Ala Ala Val Arg Ala Gly Gly Lys Gly Cys Cys Gly Ala Gly Cys  
 15 65                    70                    75                    80  
 Cys Gly Asn Arg Cys Arg Met Leu Arg Ser Val Phe Ser Ser Ala Phe  
                     85                    90                    95  
 Gly Val Leu Gly Ala Ile Tyr Cys Leu Ser Val Ser Gly Ala Gly Leu  
                     100                    105                    110  
 20 Arg Asn Gly Pro Arg Cys Leu Met Asn Gly Glu Trp Gly Tyr His Phe  
                     115                    120                    125  
 Glu Asp Thr Ala Gly Ala Tyr Leu Leu Asn Arg Thr Leu Trp Asp Arg  
                     130                    135                    140  
 Cys Glu Ala Pro Pro Arg Val Val Pro Trp Asn Val Thr Leu Phe Ser  
 25 145                    150                    155                    160  
 Leu Leu Val Ala Ala Ser Cys Leu Glu Ile Val Leu Cys Gly Ile Gln  
                     165                    170                    175  
 Leu Val Asn Ala Thr Ile Gly Val Phe Cys Gly Asp Cys Arg Lys Lys  
                     180                    185                    190  
 30 Gln Asp Thr Pro His  
                     195

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 221  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

5

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP01526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

10 Met Glu Ala Gly Gly Phe Leu Asp Ser Leu Ile Tyr Gly Ala Cys Val
    1           5           10           15
Val Phe Thr Leu Gly Met Phe Ser Ala Gly Leu Ser Asp Leu Arg His
    20           25           30
Met Arg Met Thr Arg Ser Val Asp Asn Val Gln Phe Leu Pro Phe Leu
15      35           40           45
Thr Thr Glu Val Asn Asn Leu Gly Trp Leu Ser Tyr Gly Ala Leu Lys
    50           55           60
Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu Gln
    65           70           75           80
20 Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg Val
    85           90           95
Val Leu Leu Gln Thr Ala Thr Leu Leu Gly Val Leu Leu Leu Gly Tyr
    100          105          110
Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro Glu Ala Arg Leu Gln Gln
25      115          120          125
Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser Pro
    130          135          140
Leu Ala Asp Leu Ala Lys Val Ile Gln Thr Lys Ser Thr Gln Cys Leu
    145          150          155          160
30 Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu Thr Ser Ala Ser Trp Cys
    165          170          175
Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Met Val Ser Asn Phe
    180          185          190
Pro Gly Ile Val Thr Ser Phe Ile Arg Phe Trp Leu Phe Trp Lys Tyr
35      195          200          205
Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu Leu Gln Thr
    210          215          220

```

## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251

(B) TYPE: Amino acid

5 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

## (vi) ORIGINAL SOURCE:

10 (A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10230

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

15

Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala Ile Thr Arg  
 1 5 10 15

Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly Lys Leu Gly  
 20 25 30

20 Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala Phe Leu Tyr  
 35 40 45

Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr Phe Pro Val  
 50 55 60

Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr Phe Leu Tyr  
 25 65 70 75 80

Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly Arg Pro Ala  
 85 90 95

Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile Val Ile Thr  
 100 105 110

30 Gly Leu Ala Met Asp Met Gln Leu Leu Met Ile Pro Leu Ile Met Ser  
 115 120 125

Val Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile Val Ser Phe  
 130 135 140

Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp Val Ile Leu  
 35 145 150 155 160

Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu Leu Ile Gly  
 165 170 175

Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg Tyr Pro Met



180                      185                      190  
 Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe Leu Tyr Arg  
           195                      200                      205  
 Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly Val Pro Pro  
 5            210                      215                      220  
 Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly Gly Arg His  
 225                      230                      235                      240  
 Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln  
                          245                      250

10

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106

15

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

20

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Epidermoid carcinoma

(C) CELL LINE: KB

(D) CLONE NAME: HP10389

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro Ser  
       1                      5                      10                      15  
 30 Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn Pro  
           20                      25                      30  
 Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro Val  
           35                      40                      45  
 Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Ala Leu Thr Tyr Gly Leu  
 35            50                      55                      60  
 Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met Arg  
       65                      70                      75                      80  
 Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu Gly

85

90

95

Leu Ala Val Thr Ala Met Lys Ser Arg Pro

100

105

5

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78

10

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

15

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10408

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly Ser

1

5

10

15

Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu Lys Glu

25

20

25

30

Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu Glu Leu Leu

35

40

45

Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly Thr Ser Val Thr

50

55

60

30

Leu His His Ala Arg Ser Gln His His Val Val Cys Asn Thr

65

70

75

## (2) INFORMATION FOR SEQ ID NO: 9:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

10

Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly  
 1 5 10 15  
 Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly  
 20 25 30  
 15 Gln Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala  
 35 40 45  
 Gln Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro  
 50 55 60  
 Arg Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala  
 20 65 70 75 80  
 Gln Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val  
 85 90 95  
 Ile Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His  
 100 105 110  
 25 Leu Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Lys Leu Glu Glu Lys  
 115 120 125  
 Gln Ala Arg Lys Ala Gln Arg Glu Ala Glu Glu Ala Glu Arg Glu Glu  
 130 135 140  
 Arg Lys Arg Leu Glu Ser Gln Arg Glu Ala Glu Trp Lys Lys Glu Glu  
 30 145 150 155 160  
 Glu Arg Leu Arg Leu Glu Glu Glu Gln Lys Glu Glu Glu Glu Arg Lys  
 165 170 175  
 Ala Arg Glu Glu Gln Ala Gln Arg Glu His Glu Glu Tyr Leu Lys Leu  
 180 185 190  
 35 Lys Glu Ala Phe Val Val Glu Glu Glu Gly Val Gly Glu Thr Met Thr  
 195 200 205  
 Glu Glu Gln Ser Gln Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys  
 210 215 220

[illegible]

15 (2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195  
(B) TYPE: Amino acid  
(D) TOPOLOGY: Linear

20 (ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
(B) CELL KIND: Stomach cancer  
(D) CLONE NAME: HP10413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

30  Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu
      1              5              10              15
      Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
            20              25              30
      Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
35              35              40              45
      Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp Asp Glu Pro Pro Pro
            50              55              60
      Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg

```

	65		70		75		80									
	Phe	Asp	Gly	Val	Gln	Asp	Pro	Arg	Ile	Leu	Met	Ala	Ile	Asn	Gly	Lys
			85				90				95					
	Val	Phe	Asp	Val	Thr	Lys	Gly	Arg	Lys	Phe	Tyr	Gly	Pro	Glu	Gly	Pro
5			100				105					110				
	Tyr	Gly	Val	Phe	Ala	Gly	Arg	Asp	Ala	Ser	Arg	Gly	Leu	Ala	Thr	Phe
			115				120					125				
	Cys	Leu	Asp	Lys	Glu	Ala	Leu	Lys	Asp	Glu	Tyr	Asp	Asp	Leu	Ser	Asp
			130				135					140				
10	Leu	Thr	Ala	Ala	Gln	Gln	Glu	Thr	Leu	Ser	Asp	Trp	Glu	Ser	Gln	Phe
			145				150					155				160
	Thr	Phe	Lys	Tyr	His	His	Val	Gly	Lys	Leu	Leu	Lys	Glu	Gly	Glu	Glu
					165					170					175	
	Pro	Thr	Val	Tyr	Ser	Asp	Glu	Glu	Glu	Pro	Lys	Asp	Glu	Ser	Ala	Arg
15			180						185					190		
	Lys	Asn	Asp													
			195													

20 (2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

25 (ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

30 (B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

35	Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu	Val
	1				5					10					15	
	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala	Gly	Ile
			20						25						30	

	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu	Pro	Asp	Ile	
			35					40					45				
	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn	Leu	His	Glu	Arg	
		50					55					60					
5	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg	Arg	Leu	Val	Val	Ser	
		65				70				75						80	
	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His	Ile	Asn	Pro	Asn	Lys	Thr	
					85					90					95		
	Leu	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys	Ser	Leu	Leu	Arg	Tyr	Gln	Ser	
10				100					105					110			
	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn	His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	
			115					120					125				
	Asn	Gly	Val	Thr	Asp	Ser	Leu	Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	
		130					135					140					
15	Leu	Ser	Glu	Glu	Leu	Leu	Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	
		145				150				155						160	
	His	Val	Pro	Leu	Ser	Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	
					165					170				175			
	Thr	Gln	Met	Val	Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	
20				180					185					190			
	Arg	Phe	Gln	Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	
		195					200					205					
	Phe	Leu	Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	
		210				215					220						
25	Glu	Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys	
		225				230				235						240	
	Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser	Leu	
					245				250					255			
	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser	Met	Ile	
30			260					265					270				
	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys	Thr	Trp	Ala	
		275					280					285					
	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	Lys	Leu	Tyr	Glu	
		290				295				300							
35	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	Thr	Pro	Glu	Lys	Ile	
		305				310				315						320	
	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	Cys	Glu	Thr	Val	Arg	Thr	
					325					330					335		

Ala Lys Leu Thr Pro Val Ser Ala Gln Leu Gln Asp Ile Glu Gly Lys  
                   340                  345                  350  
 Ile Asp Arg Phe Ile Ile Pro Arg Glu Thr Leu Val Leu Tyr Ala Leu  
                   355                  360                  365  
 5 Gly Val Val Leu Gln Asp Pro Asn Thr Trp Pro Ser Pro His Lys Phe  
                   370                  375                  380  
 Asp Pro Asp Arg Phe Asp Asp Glu Leu Val Met Lys Thr Phe Ser Ser  
                   385                  390                  395                  400  
 Leu Gly Phe Ser Gly Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr  
 10                  405                  410                  415  
 Met Val Thr Thr Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu  
                   420                  425                  430  
 Leu Ser Val Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr  
                   435                  440                  445  
 15 Ser Ser Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
                   450                  455                  460

## (2) INFORMATION FOR SEQ ID NO: 12:

20 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 247  
       (B) TYPE: Amino acid  
       (D) TOPOLOGY: Linear  
       (ii) SEQUENCE KIND: Protein  
 25 (iii) HYPOTHETICAL: No  
  
       (vi) ORIGINAL SOURCE:  
           (A) ORGANISM: *Homo sapiens*  
           (B) CELL KIND: Stomach cancer  
 30 (D) CLONE NAME: HP10419

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro  
 35     1                  5                  10                  15  
 Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu Arg Val  
                   20                  25                  30  
 Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu

	35		40		45											
	Ala	Ser	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr	Asp	Arg	Ser	Asp
	50				55					60						
	Ala	Arg	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly	Ala	Ala	Val	Ser	Val
5	65				70					75					80	
	Leu	Leu	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	Tyr	Lys	Leu	Leu	Lys	Lys
				85						90					95	
	Ala	Asp	Glu	Gly	Leu	Ala	Ser	Leu	Ser	Glu	Asp	Gly	Arg	Ser	Pro	Ile
			100						105						110	
10	Ser	Ile	Arg	Gln	Met	Ala	Tyr	Val	Ser	Gly	Leu	Ser	Phe	Gly	Ile	Ile
			115						120						125	
	Ser	Gly	Val	Phe	Ser	Val	Ile	Asn	Ile	Leu	Ala	Asp	Ala	Leu	Gly	Pro
			130						135						140	
	Gly	Val	Val	Gly	Ile	His	Gly	Asp	Ser	Pro	Tyr	Tyr	Phe	Leu	Thr	Ser
15	145				150					155					160	
	Ala	Phe	Leu	Thr	Ala	Ala	Ile	Ile	Leu	Leu	His	Thr	Phe	Trp	Gly	Val
				165						170					175	
	Val	Phe	Phe	Asp	Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	Ala	Leu	Gly	Leu
				180						185					190	
20	Val	Val	Gly	Ser	His	Leu	Leu	Thr	Ser	Gly	Leu	Thr	Phe	Leu	Asn	Pro
			195							200					205	
	Trp	Tyr	Glu	Ala	Ser	Leu	Leu	Pro	Ile	Tyr	Ala	Val	Thr	Val	Ser	Met
			210							215					220	
	Gly	Leu	Trp	Ala	Phe	Ile	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Ser	Ile	Gln
25	225				230					235					240	
	Arg	Ser	Leu	Leu	Cys	Lys	Asp									
				245												

## 30 (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

## 35 (ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:



(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10424

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Asn Phe Tyr Leu Leu Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile  
 1 5 10 15  
 Val Phe Trp Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser  
 10 20 25 30  
 Ser Asn Ser Thr Ala Leu Ala Leu Val Arg Pro Ser Ser Ser Gly Leu  
 35 40 45  
 Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg  
 50 55 60  
 15 Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile  
 65 70 75 80  
 Leu Val Asn Leu Ser Met Val Glu Asn Lys Leu Val Glu Leu Glu His  
 85 90 95  
 Thr Leu Leu Ser Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser  
 20 100 105 110  
 Thr

(2) INFORMATION FOR SEQ ID NO: 14:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

30 (iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Epidermoid carcinoma  
 35 (C) CELL LINE: KB  
 (D) CLONE NAME: HP10428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

	Met	Gly	Arg	Trp	Ala	Leu	Asp	Val	Ala	Phe	Leu	Trp	Lys	Ala	Val	Leu
	1				5					10					15	
	Thr	Leu	Gly	Leu	Val	Leu	Leu	Tyr	Tyr	Cys	Phe	Ser	Ile	Gly	Ile	Thr
				20					25					30		
5	Phe	Tyr	Asn	Lys	Trp	Leu	Thr	Lys	Ser	Phe	His	Phe	Pro	Leu	Phe	Met
			35					40					45			
	Thr	Met	Leu	His	Leu	Ala	Val	Ile	Phe	Leu	Phe	Ser	Ala	Leu	Ser	Arg
	50						55					60				
	Ala	Leu	Val	Gln	Cys	Ser	Ser	His	Arg	Ala	Arg	Val	Val	Leu	Ser	Trp
10	65					70				75					80	
	Ala	Asp	Tyr	Leu	Arg	Arg	Val	Ala	Pro	Thr	Ala	Leu	Ala	Thr	Ala	Leu
				85					90				95			
	Asp	Val	Gly	Leu	Ser	Asn	Trp	Ser	Phe	Leu	Tyr	Val	Thr	Val	Ser	Leu
			100						105				110			
15	Tyr	Thr	Met	Thr	Lys	Ser	Ser	Ala	Val	Leu	Phe	Ile	Leu	Ile	Phe	Ser
			115					120					125			
	Leu	Ile	Phe	Lys	Leu	Glu	Glu	Leu	Arg	Ala	Ala	Leu	Val	Leu	Val	Val
	130					135						140				
	Leu	Leu	Ile	Ala	Gly	Gly	Leu	Phe	Met	Phe	Thr	Tyr	Lys	Ser	Thr	Gln
20	145				150					155					160	
	Phe	Asn	Val	Glu	Gly	Phe	Ala	Leu	Val	Leu	Gly	Ala	Ser	Phe	Ile	Gly
				165						170				175		
	Gly	Ile	Arg	Trp	Thr	Leu	Thr	Gln	Met	Leu	Leu	Gln	Lys	Ala	Glu	Leu
			180					185					190			
25	Gly	Leu	Gln	Asn	Pro	Ile	Asp	Thr	Met	Phe	His	Leu	Gln	Pro	Leu	Met
			195					200					205			
	Phe	Leu	Gly	Leu	Phe	Pro	Leu	Phe	Ala	Val	Phe	Glu	Gly	Leu	His	Leu
	210					215						220				
	Ser	Thr	Ser	Glu	Lys	Ile	Phe	Arg	Phe	Gln	Asp	Thr	Gly	Leu	Leu	Leu
30	225				230					235				240		
	Arg	Val	Leu	Gly	Ser	Leu	Phe	Leu	Gly	Gly	Ile	Leu	Ala	Phe	Gly	Leu
				245					250				255			
	Gly	Phe	Ser	Glu	Phe	Leu	Leu	Val	Ser	Arg	Thr	Ser	Ser	Leu	Thr	Leu
			260					265					270			
35	Ser	Ile	Ala	Gly	Ile	Phe	Lys	Glu	Val	Cys	Thr	Leu	Leu	Leu	Ala	Ala
			275					280					285			
	His	Leu	Leu	Gly	Asp	Gln	Ile	Ser	Leu	Leu	Asn	Trp	Leu	Gly	Phe	Ala
			290					295					300			

Leu Cys Leu Ser Gly Ile Ser Leu His Val Ala Leu Lys Ala Leu His  
 305                      310                      315                      320  
 Ser Arg Gly Asp Gly Gly Pro Lys Ala Leu Lys Gly Leu Gly Ser Ser  
                     325                      330                      335  
 5 Pro Asp Leu Glu Leu Leu Leu Arg Ser Ser Gln Arg Glu Glu Gly Asp  
                     340                      345                      350  
 Asn Glu Glu Glu Glu Tyr Phe Val Ala Gln Gly Gln Gln  
                     355                      360                      365

10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226

(B) TYPE: Amino acid

15

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

25

Met Pro Thr Thr Lys Lys Thr Leu Met Phe Leu Ser Ser Phe Phe Thr  
   1                      5                      10                      15  
 Ser Leu Gly Ser Phe Ile Val Ile Cys Ser Ile Leu Gly Thr Gln Ala  
                     20                      25                      30  
 30 Trp Ile Thr Ser Thr Ile Ala Val Arg Asp Ser Ala Ser Asn Gly Ser  
                     35                      40                      45  
 Ile Phe Ile Thr Tyr Gly Leu Phe Arg Gly Glu Ser Ser Glu Glu Leu  
                     50                      55                      60  
 Ser His Gly Leu Ala Glu Pro Lys Lys Lys Phe Ala Val Leu Glu Ile  
 35   65                      70                      75                      80  
 Leu Asn Asn Ser Ser Gln Lys Thr Leu His Ser Val Thr Ile Leu Phe  
                     85                      90                      95  
 Leu Val Leu Ser Leu Ile Thr Ser Leu Leu Ser Ser Gly Phe Thr Phe

100 105 110  
 Tyr Asn Ser Ile Ser Asn Pro Tyr Gln Thr Phe Leu Gly Pro Thr Gly  
 115 120 125  
 Val Tyr Thr Trp Asn Gly Leu Gly Ala Ser Phe Val Phe Val Thr Met  
 5 130 135 140  
 Ile Leu Phe Val Ala Asn Thr Gln Ser Asn Gln Leu Ser Glu Glu Leu  
 145 150 155 160  
 Phe Gln Met Leu Tyr Pro Ala Thr Thr Ser Lys Gly Thr Thr His Ser  
 165 170 175  
 10 Tyr Gly Tyr Ser Phe Trp Leu Ile Leu Leu Val Ile Leu Leu Asn Ile  
 180 185 190  
 Val Thr Val Thr Ile Ile Ile Phe Tyr Gln Lys Ala Arg Tyr Gln Arg  
 195 200 205  
 Lys Gln Glu Gln Arg Lys Pro Met Glu Tyr Ala Pro Arg Asp Gly Ile  
 15 210 215 220  
 Leu Phe  
 225

20 (2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

25 (ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

30 (B) CELL KIND: Liver

(D) CLONE NAME: HP10432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

35 Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly  
 1 5 10 15  
 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly  
 20 25 30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys  
           35                          40                          45  
 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys  
           50                          55                          60  
 5 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro  
    65                          70                          75                          80  
 Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser  
                           85                          90                          95  
 Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr  
 10                          100                          105                          110  
 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile  
           115                          120                          125  
 Gln

15

## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163

20

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

25

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP10433

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly Ala Val Gly  
    1                          5                          10                          15  
 Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly Leu Gln Val  
 35                          20                          25                          30  
 Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp Ala Phe Gln  
           35                          40                          45  
 Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro Ala Gly Ile

50                                      55                                      60  
 Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys Arg Lys Arg  
 65                                      70                                      75                                      80  
 Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly Arg Lys Arg  
 5                                      85                                      90                                      95  
 Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys Val Leu Gly  
 100                                      105                                      110  
 Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg Glu Ala Glu  
 115                                      120                                      125  
 10 Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala Gly Glu Asp  
 130                                      135                                      140  
 Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser Lys Ala Leu  
 145                                      150                                      155                                      160  
 Pro Arg Ser  
 15

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193

20 (B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10480

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro  
 1                                      5                                      10                                      15  
 Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly  
 35                                      20                                      25                                      30  
 Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp  
 35                                      40                                      45  
 Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly

50                      55                      60  
 Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Met  
 65                      70                      75                      80  
 Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe  
 5                      85                      90                      95  
 Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly  
 100                      105                      110  
 Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile  
 115                      120                      125  
 10 Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Arg Ala  
 130                      135                      140  
 Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr  
 145                      150                      155                      160  
 Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr  
 15                      165                      170                      175  
 Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser  
 180                      185                      190  
 Ala

20

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146

(B) TYPE: Nucleic acid

25

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Linear

(D) CLONE NAME: HP01263

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

35

ATGGGTCTGC TCCTTCCCCT GGCACCTCTGC ATCCTAGTCC TGTGCTGCGG AGCAATGTCT 60  
 CCACCCCAGC TGGCCCTCAA CCCCTCGGCT CTGCTCTCCC GGGGCTGCAA TGA CTCCGAT 120  
 GTGCTGGCAG TTGCAGGCTT TGCCCTGCGG GATATTAACA AAGACAGAAA GGATGGCTAT 180

	GTGCTGAGAC	TCAACCGAGT	GAACGACGCC	CAGGAATACA	GACGGGGTGG	CCTGGGATCT	240
	CTGTTCTATC	TTACACTGGA	TGTGCTAGAG	ACTGACTGCC	ATGTGCTCAG	AAAGAAGGCA	300
	TGGCAAGACT	GTGGAATGAG	GATATTTTTT	GAATCAGTTT	ATGGTCAATG	CAAAGCAATA	360
	TTTTATATGA	ACAACCCAAG	TAGAGTTCTC	TATTTAGCTG	CTTATAACTG	TACTCTTCGC	420
5	CCAGTTTCAA	AAAAAAAGAT	TTACATGACG	TGCCCTGACT	GCCCAAGCTC	CATACCCACT	480
	GACTCTTCCA	ATCACCAAGT	GCTGGAGGCT	GCCACCGAGT	CTCTTGCGAA	ATACAACAAT	540
	GAGAACACAT	CCAAGCAGTA	TTCTCTCTTC	AAAGTCACCA	GGGCTTCTAG	CCAGTGGGTG	600
	GTCGGCCCTT	CTTACTTTGT	GGAATACTTA	ATTAAAGAAT	CACCATGTAC	TAAATCCCAG	660
	GCCAGCAGCT	GTTCACTTCA	GTCTCCGAC	TCTGTGCCTG	TTGGTCTTTG	CAAAGGTTCT	720
10	CTGACTCGAA	CACACTGGGA	AAAGTTTGTC	TCTGTGACTT	GTGACTTCTT	TGAATCACAG	780
	GCTCCAGCCA	CTGGAAGTGA	AAACTCTGCT	GTTAACCAGA	AACCTACAAA	CCTTCCCAAG	840
	GTGGAAGAAT	CCCAGCAGAA	AAACACCCCC	CCAACAGACT	CCCCCTCCAA	AGCTGGGCCA	900
	AGAGGATCTG	TCCAATATCT	TCCTGACTTG	GATGATAAAA	ATTCCCAGGA	AAAGGGCCCT	960
	CAGGAGGCCT	TTCCTGTGCA	TCTGGACCTA	ACCACGAATC	CCCAGGGAGA	AACCCTGGAT	1020
15	ATTTCTTCC	TCTTCCTGGA	GCCTATGGAG	GAGAAGCTGG	TTGTCCTGCC	TTTCCCCAAA	1080
	GAAAAAGCAC	GCACTGCTGA	GTGCCCAGGG	CCAGCCCAGA	ATGCCAGCCC	TCTTGTCTTT	1140
	CCGCCA						1146

20 (2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Liver
- (D) CLONE NAME: HP01299

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

35	ATGTGGCTCT	ACCTGGCGGC	CTTCGTGGGC	CTGTACTACC	TTCTGCACTG	GTACCGGGAG	60
	AGGCAGGTGG	TGAGCCACCT	CCAAGACAAG	TATGTCTTTA	TCACGGGCTG	TGACTCGGGC	120
	TTTGGGAACC	TGCTGGCCAG	ACAGCTGGAT	GCACGAGGCT	TGAGAGTGCT	GGCTGCGTGT	180
	CTGACGGAGA	AGGGGGCCGA	GCAGCTGAGG	GGCCAGACGT	CTGACAGGCT	GGAGACGGTG	240



	ACCCTGGATG	TTACCAAGAT	GGAGAGCATC	GCTGCAGCTA	CTCAGTGGGT	GAAGGAGCAT	300
	GTGGGGGACA	GAGGACTCTG	GGGACTGGTG	AACAATGCAG	GCATTCTTAC	ACCAATTACC	360
	TTATGTGAGT	GGCTGAACAC	TGAGGACTCT	ATGAATATGC	TCAAAGTGAA	CCTCATTGGT	420
	GTGATCCAGG	TGACCTTGAG	CATGCTTCCT	TTGGTGAGGA	GAGCACGGGG	AAGAATTGTC	480
5	AATGTCTCCA	GCATTCTGGG	AAGAGTTGCT	TTCTTTGTAG	GAGGCTACTG	TGTCTCCAAG	540
	TATGGAGTGG	AAGCCTTTTC	AGATATTCTG	AGGCGTGAGA	TTCAACATTT	TGGGGTGAAA	600
	ATCAGCATAG	TTGAACCTGG	CTACTTCAGA	ACGGGAATGA	CAAACATGAC	ACAGTCCTTA	660
	GAGCGAATGA	AGCAAAGTTG	GAAAGAAGCC	CCCAAGCATA	TTAAGGAGAC	CTATGGACAG	720
	CAGTATTTTG	ATGCCCTTTA	CAATATCATG	AAGGAAGGGC	TGTTGAATTG	TAGCACAAAC	780
10	CTGAACCTGG	TCACTGACTG	CATGGAACAT	GCTCTGACAT	CGGTGCATCC	GCGAACTCGA	840
	TATTCAGCTG	GCTGGGATGC	TAAATTTTTC	TTCATCCCTC	TATCTTATTT	ACCTACATCA	900
	CTGGCAGACT	ACATTTTGAC	TAGATCTTGG	CCCAAACCAG	CCCAGGCAGT	C	951

## 15 (2) INFORMATION FOR SEQ ID NO: 21:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Liver

(D) CLONE NAME: HP01347

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

30	ATGAGTGACT	CCAAGGAACC	AAGGGTGACG	CAGCTGGGCC	TCCTGGGGTG	TCTTGCCCAT	60
	GGCGCCCTGG	TGCTGCAACT	CCTCTCCTTC	ATGCTCTTGG	CTGGGGTCCT	GGTGGCCATC	120
	CTTGTCCAAG	TGTCCAAGGT	CCCCAGCTCC	CTAAGTCAGG	AACAATCCGA	GCAAGACGCA	180
	ATCTACCAGA	ACCTGACCCA	GCTTAAAGCT	GCAGTGGGTG	AGCTCTCAGA	GAAATCCAAG	240
	CTGCAGGAGA	TCTACCAGGA	GCTGACCCAG	CTGAAGGCTG	CAGTGGGTGA	GTTGCCAGAG	300
35	AAATCCAAGC	TGCAGGAGAT	CTACCAGGAG	CTGACCCGGC	TGAAGGCTGC	AGTGGGTGAG	360
	TTGCCAGAGA	AATCCAAGCT	GCAGGAGATC	TACCAGGAGC	TGACCCGGCT	GAAGGCTGCA	420
	GTGGGTGAGT	TGCCAGAGAA	ATCCAAGCTG	CAGGAGATCT	ACCAGGAGCT	GACCCGGCTG	480
	AAGGCTGCAG	TGGGTGAGTT	GCCAGAGAAA	TCCAAGCTGC	AGGAGATCTA	CCAGGAGCTG	540

ACGGAGCTGA AGGCTGCAGT GGGTGAGTTG CCAGAGAAAT CCAAGCTGCA GGAGATCTAC 600  
 CAGGAGCTGA CCCAGCTGAA GGCTGCAGTG GGTGAGTTGC CAGACCAGTC CAAGCAGCAG 660  
 CAAATCTATC AAGAACTGAC CGATTTGAAG ACTGCATTTG AACGCCTGTG CCGCCACTGT 720  
 CCCAAGGACT GGACATTCTT CCAAGGAAAC TGTTACTTCA TGTCTAACTC CCAGCGGAAC 780  
 5 TGGCACGACT CCGTCACCGC CTGCCAGGAA GTGAGGGCCC AGCTCGTCGT AATCAAAACT 840  
 GCTGAGGAGC AGCTTCCAGC GGTACTGGAA CAGTGGAGAA CCCAACAA 888

## (2) INFORMATION FOR SEQ ID NO: 22:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 591  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear  
 15 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 20 (D) CLONE NAME: HP01440

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

ATGTGTACGG GAAAATGTGC CCGCTGTGTG GGGCTCTCCC TCATTACCCT CTGCCTCGTC 60  
 25 TGCATTGTGG CCAACGCCCT CCTGCTGGTA CCTAATGGGG AGACCTCCTG GACCAACACC 120  
 AACCATCTCA GCTTGCAAGT CTGGCTCATG GGCGGCTTCA TTGGCGGGGG CCTAATGGTA 180  
 CTGTGTCCGG GGATTGCAGC CGTTCGGGCA GGGGGCAAGG GCTGCTGTGG TGCTGGGTGC 240  
 TGTGGAAACC GCTGCAGGAT GCTGCGCTCG GTCTTCTCCT CGGCGTTCGG GGTGCTTGGT 300  
 GCCATCTACT GCCTCTCGGT GTCTGGAGCT GGGCTCCGAA ATGGACCCAG ATGCTTAATG 360  
 30 AACGGCGAGT GGGGCTACCA CTTCGAAGAC ACCGCGGGAG CTTACTTGCT CAACCGCACT 420  
 CTATGGGATC GGTGCGAGGC GCCCCCTCGC GTGGTCCCCT GGAATGTGAC GCTCTTCTCG 480  
 CTGCTGGTGG CCGCCTCCTG CCTGGAGATA GTACTGTGTG GGATCCAGCT GGTGAACGCG 540  
 ACCATTGGTG TCTTCTGCGG CGATTGCAGG AAAAAACAGG ACACCCCTCA C 591

35

## (2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 663

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP01526

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

	ATGGAGGCGG GCGGCTTTCT GGA	CTCGCTC	ATTTACGGAG	CATGCGTGGT	CTTCACCCTT	60
	GGCATGTTCT CCGCCGGCCT CTC	GGACCTC	AGGCACATGC	GAATGACCCG	GAGTGTGGAC	120
15	AACGTCCAGT TCCTGCCCTT TCT	CACCACG	GAAGTCAACA	ACCTGGGCTG	GCTGAGTTAT	180
	GGGGCTTTGA AGGGAGACGG GAT	CCTCATC	GTCGTCAACA	CAGTGGGTGC	TGCGCTTCAG	240
	ACCCTGTATA TCTTGGCATA TCT	GCATTAC	TGCCCTCGGA	AGCGTGTGT	GCTCCTACAG	300
	ACTGCAACCC TGCTAGGGGT CCT	TCTCCTG	GGTTATGGCT	ACTTTTGGCT	CCTGGTACCC	360
	AACCCTGAGG CCCGGCTTCA GC	AGTTGGGC	CTCTTCTGCA	GTGTCTTCAC	CATCAGCATG	420
20	TACCTCTCAC CACTGGCTGA CTT	GGCTAAG	GTGATTCAAA	CTAAATCAAC	CCAATGTCTC	480
	TCCTACCCAC TCACCATTGC TAC	CCTTCTC	ACCTCTGCCT	CCTGGTGCCT	CTATGGGTTT	540
	CGACTCAGAG ATCCCTATAT CAT	GGTGTCC	AACTTTCCAG	GAATCGTCAC	CAGCTTTATC	600
	CGCTTCTGGC TTTTCTGGAA GT	ACCCCCAG	GAGCAAGACA	GGAACTACTG	GCTCCTGCAA	660
	ACC					663

25

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 753

30

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10230

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

	ATGTCGGACA	TCGGAGACTG	G TTCAGGAGC	ATCCCGGCGA	TCACGCGCTA	TTGGTTCGCC	60
	GCCACCGTCG	CCGTGCCCTT	GGTCGGCAAA	CTCGGCCTCA	TCAGCCCGGC	CTACCTCTTC	120
5	CTCTGGCCCCG	AAGCCTTCCT	TTATCGCTTT	CAGATTTGGA	GGCCAATCAC	TGCCACCTTT	180
	TATTTCCCTG	TGGGTCCAGG	AACTGGATTT	CTTTATTTGG	TCAATTTATA	TTTCTTATAT	240
	CAGTATTCTA	CGCGACTTGA	AACAGGAGCT	TTTGATGGGA	GGCCAGCAGA	CTATTTATTC	300
	ATGCTCCTCT	TTAACTGGAT	TTGCATCGTG	ATTACTGGCT	TAGCAATGGA	TATGCAGTTG	360
	CTGATGATTC	CTCTGATCAT	GTCAGTACTT	TATGTCTGGG	CCCAGCTGAA	CAGAGACATG	420
10	ATTGTATCAT	TTTGGTTTGG	AACACGATTT	AAGGCCTGCT	ATTTACCCTG	GGTTATCCTT	480
	GGATTCAACT	ATATCATCGG	AGGCTCGGTA	ATCAATGAGC	TTATTGGAAA	TCTGGTTGGA	540
	CATCTTTATT	TTTTCCTAAT	G TTCAGATAC	CCAATGGACT	TGGGAGGAAG	AAATTTTCTA	600
	TCCACACCTC	AGTTTTTGTG	CCGCTGGCTG	CCCAGTAGGA	GAGGAGGAGT	ATCAGGATTT	660
	GGTG TGCCCC	CTGCTAGCAT	GAGGCGAGCT	GCTGATCAGA	ATGGCGGAGG	CGGGAGACAC	720
15	AACTGGGGCC	AGGGCTTTTCG	ACTTGGAGAC	CAG			753

## (2) INFORMATION FOR SEQ ID NO: 25:

## (i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 318
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

25

## (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Homo sapiens</i>
	(B) CELL KIND: Epidermoid carcinoma
	(C) CELL LINE: KB
30	(D) CLONE NAME: HP10389

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

	ATGGCGACTC	CCGGCCCTGT	GATTCCGGAG	GTCCCCTTTG	AACCATCGAA	GCCTCCAGTC	60
35	ATTGAGGGGC	TGAGCCCCAC	TGTTTACAGG	AATCCAGAGA	GTTTCAAGGA	AAAGTTTCGT	120
	CGCAAGACCC	GCGAGAACCC	GGTGGTACCC	ATAGGTTGCC	TGGCCACGGC	GGCCGCCCTC	180
	ACCTACGGCC	TCTACTCCTT	CCACCGGGGC	AACAGCCAGC	GCTCTCAGCT	CATGATGCGC	240
	ACCCGGATCG	CCGCCCAGGG	TTTCACGGTC	GCAGCCATCT	TGCTGGGTCT	GGCTGTCACT	300

GCTATGAAGT CTCGACCC

318

## (2) INFORMATION FOR SEQ ID NO: 26:

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 10 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10408

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ATGGGGTCTG	GGCTGCCCCT	TGTCCTCCTC	TTGACCCTCC	TTGGCAGCTC	ACATGGAACA	60
20 GGGCCGGGTA	TGACTTTGCA	ACTGAAGCTG	AAGGAGTCTT	TTCTGACAAA	TTCCTCCTAT	120
GAGTCCAGCT	TCCTGGAATT	GCTTGAAAAG	CTCTGCCTCC	TCCTCCATCT	CCCTTCAGGG	180
ACCAGCGTCA	CCCTCCACCA	TGCAAGATCT	CAACACCATG	TTGTCTGCAA	CACA	234

## 25 (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 942
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 30 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10412

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

	ATGGTGGCGC	CTGTGTGGTA	CTTGGTAGCG	GCGGCTCTGC	TAGTCGGCTT	TATCCTCTTC	60
	CTGACTCGCA	GCCGGGGCCG	GGCGGCATCA	GCCGGCCAAG	AGCCACTGCA	CAATGAGGAG	120
	CTGGCAGGAG	CAGGCCGGGT	GGCCCAGCCT	GGGCCCCTGG	AGCCTGAGGA	GCCGAGAGCT	180
	GGAGGCAGGC	CTCGGCGCCG	GAGGGACCTG	GGCAGCCGCC	TACAGGCCCA	GCGTCGAGCC	240
5	CAGCGGGTGG	CCTGGGCAGA	AGCAGATGAG	AACGAGGAGG	AAGCTGTCAT	CCTAGCCCAG	300
	GAGGAGGAAG	GTGTGAGAAA	GCCAGCGGAA	ACTCACCTGT	CGGGGAAAAT	TGGAGCTAAG	360
	AAACTGCGGA	AGCTGGAGGA	GAAACAAGCG	CGAAAGGCCC	AGCGTGAGGC	AGAGGAGGCT	420
	GAACGTGAGG	AGCGGAAACG	ACTCGAGTCC	CAGCGCGAAG	CTGAGTGGA	GAAGGAGGAG	480
	GAGCGGCTTC	GCCTGGAGGA	GGAGCAGAAG	GAGGAGGAGG	AGAGGAAGGC	CCGCGAGGAG	540
10	CAGGCCCAGC	GGGAGCATGA	GGAGTACCTG	AAACTGAAGG	AGGCCTTTGT	GGTGGAGGAG	600
	GAAGGCGTAG	GAGAGACCAT	GAAGTACCTG	CAGTCCCAGA	GCTTCCTGAC	AGAGTTCATC	660
	AACTACATCA	AGCAGTCCAA	GGTTGTGCTC	TTGGAAGACC	TGGCTTCCA	GGTGGGCCTA	720
	CGCACTCAGG	ACACCATAAA	TCGCATCCAG	GACCTGCTGG	CTGAGGGGAC	TATAACAGGT	780
	GTGATTGACG	ACCGGGGCAA	GTTTCATCTAC	ATAACCCAG	AGGAACTGGC	CGCCGTGGCC	840
15	AACTTCATCC	GACAGCGGGG	CCGGGTGTCC	ATCGCCGAGC	TTGCCCAAGC	CAGCAACTCC	900
	CTCATCGCCT	GGGGCCGGGA	GTCCCCTGCC	CAAGCCCCAG	CC		942

## (2) INFORMATION FOR SEQ ID NO: 28:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 585
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 25 (ii) SEQUENCE KIND: cDNA to mRNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Homo sapiens*
  - (B) CELL KIND: Stomach cancer
  - (D) CLONE NAME: HP10413
- 30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

	ATGGCTGCCG	AGGATGTGGT	GGCGACTGGC	GCCGACCCAA	GCGATCTGGA	GAGCGGCGGG	60
35	CTGCTGCATG	AGATTTTTCAC	GTGCGCGCTC	AACCTGCTGC	TGCTTGGCCT	CTGCATCTTC	120
	CTGCTCTACA	AGATCGTGCG	CGGGGACCAG	CCGGCGGCCA	GCGGCGACAG	CGACGACGAC	180
	GAGCCGCCCC	CTCTGCCCCG	CCTCAAGCGG	CGCGACTTCA	CCCCCGCCGA	GCTGCGGCGC	240
	TTCGACGGCG	TCCAGGACCC	GCGCATACTC	ATGGCCATCA	ACGGCAAGGT	GTTTCATGTG	300

	ACCAAAGGCC	GCAAATTCTA	CGGGCCCCGAG	GGGCCGTATG	GGGTCTTTGC	TGGAAGAGAT	360
	GCATCCAGGG	GCCTTGCCAC	ATTTTGCCTG	GATAAGGAAG	CACTGAAGGA	TGAGTACGAT	420
	GACCTTTCTG	ACCTCACTGC	TGCCCAGCAG	GAGACTCTGA	GTGACTGGGA	GTCTCAGTTC	480
	ACTTTCAAGT	ATCATCACGT	GGGCAAACCTG	CTGAAGGAGG	GGGAGGAGCC	CACTGTGTAC	540
5	TCAGATGAGG	AAGAACCAAA	AGATGAGAGT	GCCCGGAAAA	ATGAT		585

## (2) INFORMATION FOR SEQ ID NO: 29:

## (i) SEQUENCE CHARACTERISTICS:

10	(A) LENGTH: 1386
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear
	(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Homo sapiens</i>
	(B) CELL KIND: Stomach cancer
	(D) CLONE NAME: HP10415

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

	ATGTTGGA	CTTCG	ATCTT	CGCCG	TTACC	TTCTTG	CTGG	CGTTGG	TGGG	AGCCGT	GGCTC	60		
	TACCTCT	ATC	CGGCTT	CCAG	ACAAGCT	GCA	GGAATT	CCAG	GGATTAC	TCC	AACTGA	AAGAA	120	
25	AAAGATG	GTA	ATCTTCC	CAGA	TATTGT	GAA	AT	AGTGGA	AGTT	TGCATG	AGTT	CCTGGT	TAA	180
	TTGCATG	GAGA	GATATGG	GCC	TGTGGT	CTCC	TTCTGG	TTTG	GCAGGC	GCCT	CGTGGT	TAGT	240	
	TTGGGCA	CTG	TTGATGT	ACT	GAAGCAG	CAT	ATCAAT	CCCA	ATAAGAC	ATT	GGACCCT	TTTT	300	
	GAAACCA	TGC	TGAAGTC	ATT	ATTAAGG	TAT	CAATCT	GGTG	GTGGCAG	TGT	GAGTGAAA	AAC	360	
	CACATGA	GGA	AAAAATT	GTA	TGAAAAT	GGT	GTGACT	GATT	CTCTGA	AAGAG	TAACTTT	TGCC	420	
30	CTCCTC	CCTAA	AGCTTT	CAGA	AGAATT	TATTA	GATAAA	TGGC	TCTCCT	ACCC	AGAGAC	CCCAG	480	
	CACGTG	CCCC	TCAGCC	CAGCA	TATGCT	TGGT	TTTGCT	TATGA	AGTCTG	TAC	ACAGAT	GGTA	540	
	ATGGGT	AGTA	CATTTGA	AGA	TGATCAG	GAA	GTCATT	CGCT	TCCAGA	AAGAA	TCATGG	CACA	600	
	GTTTGG	TCTG	AGATTGG	AAA	AGGCTTT	CTA	GATGGG	TCAC	TTGATA	AAAAA	CATGACT	CGG	660	
	AAAAAAC	CAAT	ATGAAG	ATGC	CCTCAT	GCAA	CTGGAG	TCTG	TTTAA	GGAA	CATCATA	AAAAA	720	
35	GAACGAA	AAAG	GAAGGAA	CTT	CAGTCA	ACAT	ATTTTC	ATTG	ACTCCT	TAGT	ACAAGG	GAAC	780	
	CTTAAT	GACC	AACAGAT	CCCT	AGAAGAC	AGT	ATGATAT	TTTT	CTCTGG	CCAG	TTGCATA	AATA	840	
	ACTGCAA	AAAT	TGTGTAC	CTG	GGCAAT	CTGT	TTTTTA	ACCA	CCTCTG	AAGA	AGTTCA	AAAAA	900	
	AAATTAT	ATG	AAGAGAT	AAA	CCAAGT	TTTTT	GGAAAT	TGGT	CTGTTAC	TCC	AGAGAAA	AATT	960	

	GAGCAGCTCA	GATATTGTCA	GCATGTGCTT	TGTGAAACTG	TTCGAACTGC	CAAACCTGACT	1020
	CCAGTTTCTG	CCCAGCTTCA	AGATATTGAA	GGAAAAATTG	ACCGATTTAT	TATTCCTAGA	1080
	GAGACCCTCG	TCCTTTATGC	CCTTGGTGTG	GTACTTCAGG	ATCCTAATAC	TTGGCCATCT	1140
	CCACACAAGT	TTGATCCAGA	TCGGTTTGAT	GATGAATTAG	TAATGAAAAC	TTTTTCCTCA	1200
5	CTTGGATTCT	CAGGCACACA	GGAGTGTCCA	GAGTTGAGGT	TTGCATATAT	GGTGACCACA	1260
	GTACTTCTTA	GTGTATTGGT	GAAGAGACTG	CACCTACTTT	CTGTGGAGGG	ACAGGTTATT	1320
	GAAACAAAGT	ATGAACTGGT	AACATCATCA	AGGGAAGAAG	CTTGGATCAC	TGTCTCAAAG	1380
	AGATAT						1386

10

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 741

(B) TYPE: Nucleic acid

15

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

25

	ATGGGGGCTG	CGGTGTTTTT	CGGCTGCACT	TTCGTGCGGT	TCGGCCCCGGC	CTTCGCGCTT	60
	TTCTTGATCA	CTGTGGCTGG	GGACCCGCTT	CGCGTTATCA	TCCTGGTCGC	AGGGGCATTT	120
	TTCTGGCTGG	TCTCCCTGCT	CCTGGCCTCT	GTGGTCTGGT	TCATCTTGGT	CCATGTGACC	180
	GACCGGTCAG	ATGCCCCGGCT	CCAGTACGGC	CTCCTGATTT	TTGGTGCTGC	TGTCTCTGTC	240
30	CTTCTACAGG	AGGTGTTCCG	CTTTGCCTAC	TACAAGCTGC	TTAAGAAGGC	AGATGAGGGG	300
	TTAGCATCGC	TGAGTGAGGA	CGGAAGATCA	CCCATCTCCA	TCCGCCAGAT	GGCCTATGTT	360
	TCTGGTCTCT	CCTTCGGTAT	CATCAGTGGT	GTCTTCTCTG	TTATCAATAT	TTTGGCTGAT	420
	GCACTTGGGC	CAGGTGTGGT	TGGGATCCAT	GGAGACTCAC	CCTATTACTT	CCTGACTTCA	480
	GCCTTTCTGA	CAGCAGCCAT	TATCCTGCTC	CATACCTTTT	GGGGAGTTGT	GTTCTTTGAT	540
35	GCCTGTGAGA	GGAGACGGTA	CTGGGCTTTG	GGCCTGGTGG	TTGGGAGTCA	CCTACTGACA	600
	TCGGGACTGA	CATTCTGAA	CCCCTGGTAT	GAGGCCAGCC	TGCTGCCCAT	CTATGCAGTC	660
	ACTGTTTCCA	TGGGGCTCTG	GGCCTTCATC	ACAGCTGGAG	GGTCCCTCCG	AAGTATTCAG	720
	CGCAGCCTCT	TGTGTAAGGA	C				741



## (2) INFORMATION FOR SEQ ID NO: 31:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339

5 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## 10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10424

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGAACTTCT	ATTTACTCCT	AGCGAGCAGC	ATTCTGTGTG	CCTTGATTGT	CTTCTGGAAA	60
TATCGCCGCT	TTCAGAGAAA	CACTGGCGAA	ATGTCATCAA	ATTCAACTGC	TCTTGCACTA	120
GTGAGACCCT	CTTCTTCTGG	GTTAATTAAC	AGCAATACAG	ACAACAATCT	TGCAGTCTAC	180
20 GACCTCTCTC	GGGATATTTT	AAATAATTTT	CCACACTCAA	TAGCCAGGCA	GAAGCGAATA	240
TTGGTAAACC	TCAGTATGGT	GGAAAACAAG	CTGGTTGAAC	TGGAACATAC	TCTACTTAGC	300
AAGGGTTTCA	GAGGTGCATC	ACCTCACCGG	AAATCCACC			339

## 25 (2) INFORMATION FOR SEQ ID NO: 32:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1095

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

35 (B) CELL KIND: Epidermoid carcinoma

(C) CELL LINE: KB

(D) CLONE NAME: HP10428

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

	ATGGGGAGGT	GGGCCCTCGA	TGTGGCCTTT	TTGTGGAAGG	CGGTGTTGAC	CCTGGGGCTG	60
	GTGCTTCTCT	ACTACTGCTT	CTCCATCGGC	ATCACCTTCT	ACAACAAGTG	GCTGACAAAG	120
5	AGCTTCCATT	TCCCCCTCTT	CATGACGATG	CTGCACCTGG	CCGTGATCTT	CCTCTTCTCC	180
	GCCCTGTCCA	GGGCGCTGGT	TCAGTGCTCC	AGCCACAGGG	CCCGTGTGGT	GCTGAGCTGG	240
	GGCGACTACC	TCAGAAGAGT	GGCTCCCACA	GCTCTGGCGA	CGGCGCTTGA	CGTGGGCTTG	300
	TCCAACTGGA	GCTTCCTGTA	TGTCACCGTC	TCGCTGTACA	CAATGACCAA	ATCCTCAGCT	360
	GTCTCTTCA	TCTTGATCTT	CTCTCTGATC	TTCAAGCTGG	AGGAGCTGCG	CGCGGCACTG	420
10	GTCTTGGTGG	TCCTCCTCAT	CGCCGGGGGT	CTCTTCATGT	TCACCTACAA	GTCCACACAG	480
	TTCAACGTGG	AGGGCTTCGC	CTTGGTGCTG	GGGGCCTCGT	TCATCGGTGG	CATTGCTGG	540
	ACCCTCACCC	AGATGCTCCT	GCAGAAGGCT	GAAGCTCGGC	TCCAGAATCC	CATCGACACC	600
	ATGTTCCACC	TGCAGCCACT	CATGTTCTTG	GGGCTCTTCC	CTCTCTTTGC	TGTATTTGAA	660
	GGTCTCCATT	TGTCCACATC	TGAGAAAATC	TTCCGTTTCC	AGGACACAGG	GCTGCTCCTG	720
15	CGGGTACTTG	GGAGCCTCTT	CCTTGGCGGG	ATTCTCGCCT	TTGGTTTGGG	CTTCTCTGAG	780
	TTCTCCTGG	TCTCCAGAAC	CTCCAGCCTC	ACTCTCTCCA	TTGCCGGCAT	TTTTAAGGAA	840
	GTCTGCACTT	TGCTGTTGGC	AGCTCATCTG	CTGGGCGATC	AGATCAGCCT	CCTGAACTGG	900
	CTGGGCTTCG	CCCTCTGCCT	CTCGGGAATA	TCCCTCCACG	TTGCCCTCAA	AGCCCTGCAT	960
	TCCAGAGGTG	ATGGTGGCCC	CAAGGCCTTG	AAGGGGCTGG	GCTCCAGCCC	CGACCTGGAG	1020
20	CTGCTGCTCC	GGAGCAGCCA	GCGGGAGGAA	GGTGACAATG	AGGAGGAGGA	GTACTTTGTG	1080
	GCCCAGGGGC	AGCAG					1095

## (2) INFORMATION FOR SEQ ID NO: 33:

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 30 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10429

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATGCCTACCA CAAAGAAGAC ATTGATGTTT TTATCAAGCT TTTTCACCAG CCTTGGGTCC 60  
 TTCATTGTAA TTTGCTCTAT TCTTGGGACA CAAGCATGGA TCACCAGTAC AATTGCTGTT 120  
 AGAGACTCTG CTTCAAATGG GAGCATTTTC ATCACTTACG GACTTTTTTCG TGGGGAGAGT 180  
 AGTGAAGAAT TGAGTCACGG ACTTGCAGAA CCAAAGAAAA AGTTTGCAGT TTTAGAGATA 240  
 5 CTGAATAATT CTTCCCAAAA AACTCTGCAT TCGGTGACTA TCCTGTTTCT GGTCTGAGT 300  
 TTGATCACGT CGCTGCTGAG CTCTGGGTTT ACCTTCTACA ACAGCATCAG CAACCCTTAC 360  
 CAGACATTCC TGGGGCCGAC GGGGGTGTAC ACCTGGAACG GGCTCGGTGC ATCCTTCGTT 420  
 TTTGTGACCA TGATACTGTT TGTGGCGAAC ACGCAGTCCA ACCAACTCTC CGAAGAGTTG 480  
 TTCCAAATGC TTTACCCGGC AACCACCAGT AAAGGAACGA CCCACAGTTA CGGATACTCG 540  
 10 TTCTGGCTCA TACTGCTCGT CATTCTTCTA AATATAGTCA CTGTAACCAT CATCATTTTC 600  
 TACCAGAAGG CCAGATACCA GCGGAAGCAG GAGCAGAGAA AGCCAATGGA ATATGCTCCA 660  
 AGGGACGGAA TTTTATTC 678

15 (2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Liver

(D) CLONE NAME: HP10432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

30 ATGGCTCGGG GCTCGCTGCG CCGGTTGCTG CGGCTCCTCG TGCTGGGGCT CTGGCTGGCG 60  
 TTGCTGCGCT CCGTGGCCGG GGAGCAAGCG CCAGGCACCG CCCCCTGCTC CCGCGGCAGC 120  
 TCCTGGAGCG CGGACCTGGA CAAGTGCATG GACTGCGCGT CTTGCAGGGC GCGACCGCAC 180  
 AGCGACTTCT GCCTGGGCTG CGCTGCAGCA CCTCCTGCCC CCTTCCGGCT GCTTTGGCCC 240  
 35 ATCCTTGGGG GCGCTCTGAG CCTGACCTTC GTGCTGGGGC TGCTTTCTGG CTTTTGGTTC 300  
 TGGAGACGAT GCCGCAGGAG AGAGAAGTTC ACCACCCCCA TAGAGGAGAC CGGCGGAGAG 360  
 GGCTGCCCAG CTGTGGCGCT GATCCAG 387

## (2) INFORMATION FOR SEQ ID NO: 35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
(B) CELL KIND: Liver  
(D) CLONE NAME: HP10433

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATGCGACGGC TGCTGATCCC TCTGGCCCTG TGGCTGGGCG CGGTGGGCGT GGGCGTCGCC 60  
GAGCTCACGG AAGCCCAGCG CCGGGGCCTG CAGGTGGCCC TGGAGGAATT TCACAAGCAC 120  
CCGCCCCTGC AGTGGGCCTT CCAGGAGACC AGTGTGGAGA GCGCCGTGGA CACGCCCTTC 180  
CCAGCTGGAA TATTTGTGAG GCTGGAATTT AAGCTGCAGC AGACAAGCTG CCGGAAGAGG 240  
GACTGGAAGA AACCCGAGTG CAAAGTCAGG CCCAATGGGA GGAAACGGAA ATGCCTGGCC 300  
TGCATCAAAC TGGGCTCTGA GGACAAAGTT CTGGGCCGGT TGGTCCACTG CCCCATAGAG 360  
ACCCAAGTTC TGCGGGAGGC TGAGGAGCAC CAGGAGACCC AGTGCCTCAG GGTGCAGCGG 420  
GCTGGTGAGG ACCCCCACAG CTTCTACTTC CCTGGACAGT TCGCCTTCTC CAAGGCCCTG 480  
CCCCGCAGC 489

## (2) INFORMATION FOR SEQ ID NO: 36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
(B) CELL KIND: Stomach cancer  
(D) CLONE NAME: HP10480

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ATGATCCGCT GCGGCCTGGC CTGCGAGCGC TGCCGCTGGA TCCTGCCCCT GCTCCTACTC 60  
 AGCGCCATCG CCTTCGACAT CATCGCGCTG GCCGGCCGCG GCTGGTTGCA GTCTAGCGAC 120  
 5 CACGGCCAGA CGTCCTCGCT GTGGTGGAAA TGCTCCCAAG AGGGCGGCGG CAGCGGGTCC 180  
 TACGAGGAGG GCTGTCAGAG CCTCATGGAG TACGCGTGGG GTAGAGCAGC GGCTGCCATG 240  
 CTCTTCTGTG GCTTCATCAT CCTGGTGATC TGTTTCATCC TCTCCTTCTT CGCCCTCTGT 300  
 GGACCCAGA TGCTTGTCTT CCTGAGAGTG ATTGGAGGTC TCCTTGCCCTT GGCTGCTGTG 360  
 TTCCAGATCA TCTCCCTGGT AATTTACCCC GTGAAGTACA CCCAGACCTT CACCCTTCAT 420  
 10 GCCAACCGTG CTGTCACTTA CATCTATAAC TGGGCCTACG GCTTTGGGTG GGCAGCCACG 480  
 ATTATCCTGA TCGGCTGTGC CTTCTTCTTC TGCTGCCTCC CCAACTACGA AGATGACCTT 540  
 CTGGGCAATG CCAAGCCCAG GTACTTCTAC ACATCTGCC 579

## 15 (2) INFORMATION FOR SEQ ID NO: 37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1502  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 20 (D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 25 (B) CELL KIND: Liver  
 (D) CLONE NAME: HP01263

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 30 (B) EXISTENCE POSITION: 37.. 1185  
 (C) CHARACTERIZATION METHOD: E

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

35 ACAAAGTGAC CCATCCTGGG CCTTGTCTC CACAGA ATG GGT CTG CTC CTT CCC 54  
 Met Gly Leu Leu Leu Pro  
 1 5  
 CTG GCA CTC TGC ATC CTA GTC CTG TGC TGC GGA GCA ATG TCT CCA CCC 102

— — —

	CCA TGT ACT AAA TCC CAG GCC AGC AGC TGT TCA CTT CAG TCC TCC GAC	726
	Pro Cys Thr Lys Ser Gln Ala Ser Ser Cys Ser Leu Gln Ser Ser Asp	
	215 220 225 230	
	TCT GTG CCT GTT GGT CTT TGC AAA GGT TCT CTG ACT CGA ACA CAC TGG	774
5	Ser Val Pro Val Gly Leu Cys Lys Gly Ser Leu Thr Arg Thr His Trp	
	235 240 245	
	GAA AAG TTT GTC TCT GTG ACT TGT GAC TTC TTT GAA TCA CAG GCT CCA	822
	Glu Lys Phe Val Ser Val Thr Cys Asp Phe Phe Glu Ser Gln Ala Pro	
	250 255 260	
10	GCC ACT GGA AGT GAA AAC TCT GCT GTT AAC CAG AAA CCT ACA AAC CTT	870
	Ala Thr Gly Ser Glu Asn Ser Ala Val Asn Gln Lys Pro Thr Asn Leu	
	265 270 275	
	CCC AAG GTG GAA GAA TCC CAG CAG AAA AAC ACC CCC CCA ACA GAC TCC	918
	Pro Lys Val Glu Glu Ser Gln Gln Lys Asn Thr Pro Pro Thr Asp Ser	
15	280 285 290	
	CCC TCC AAA GCT GGG CCA AGA GGA TCT GTC CAA TAT CTT CCT GAC TTG	966
	Pro Ser Lys Ala Gly Pro Arg Gly Ser Val Gln Tyr Leu Pro Asp Leu	
	295 300 305 310	
	GAT GAT AAA AAT TCC CAG GAA AAG GGC CCT CAG GAG GCC TTT CCT GTG	1014
20	Asp Asp Lys Asn Ser Gln Glu Lys Gly Pro Gln Glu Ala Phe Pro Val	
	315 320 325	
	CAT CTG GAC CTA ACC ACG AAT CCC CAG GGA GAA ACC CTG GAT ATT TCC	1062
	His Leu Asp Leu Thr Thr Asn Pro Gln Gly Glu Thr Leu Asp Ile Ser	
	330 335 340	
25	TTC CTC TTC CTG GAG CCT ATG GAG GAG AAG CTG GTT GTC CTG CCT TTC	1110
	Phe Leu Phe Leu Glu Pro Met Glu Glu Lys Leu Val Val Leu Pro Phe	
	345 350 355	
	CCC AAA GAA AAA GCA CGC ACT GCT GAG TGC CCA GGG CCA GCC CAG AAT	1158
	Pro Lys Glu Lys Ala Arg Thr Ala Glu Cys Pro Gly Pro Ala Gln Asn	
30	360 365 370	
	GCC AGC CCT CTT GTC CTT CCG CCA TGAGAATCAC ACAGAGTCTT CTGTAGGG	1210
	Ala Ser Pro Leu Val Leu Pro Pro	
	375 380	
	GTATGGTGCG CCGCATGACA TGGGAGGCCA TGGGGACGAT GGACAGAGAC AGAGCGTGCA	1270
35	CACGTAGAGT GGCTAGTGAA GGACGCCTTT TTGACTCTTC TTGGTCTCAG CATGTTGACT	1330
	GGGATTGGAA ATAATGAGAC TGAGCCCTCG GCTTGGGCTG CACTCTACCC TGTACACTGC	1390
	CTTGTACCCT GAGCTGCATC ACCTCCTAAA CTGAGCAGTC TCATACCATG GAGAGATGCC	1450
	TCTCTTATGT CTTAGCCAC TCACTTATAA AGATACTTAT CTTTTCAGCA GT	1502

## (2) INFORMATION FOR SEQ ID NO: 38:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1349

5 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## 10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP01299

15

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 111.. 1064

(C) CHARACTERIZATION METHOD: E

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

AGCAGTTGGG GCAGGAGGAA GCCGACTGCT GCCTGGTCTG CAAAGAAGTC CTTTCAAGTC      60
TCTAGGACTG GACTCTTCCT AAGCAAGTCC GAGAAGGAAG CACCCTCACT ATG TGG      116
25                                     Met Trp
                                     1
CTC TAC CTG GCG GCC TTC GTG GGC CTG TAC TAC CTT CTG CAC TGG TAC
164
Leu Tyr Leu Ala Ala Phe Val Gly Leu Tyr Tyr Leu Leu His Trp Tyr
30          5              10              15
CGG GAG AGG CAG GTG GTG AGC CAC CTC CAA GAC AAG TAT GTC TTT ATC      212
Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val Phe Ile
          20              25              30
ACG GGC TGT GAC TCG GGC TTT GGG AAC CTG CTG GCC AGA CAG CTG GAT      260
35 Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln Leu Asp
          35              40              45              50
GCA CGA GGC TTG AGA GTG CTG GCT GCG TGT CTG ACG GAG AAG GGG GCC      308
Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys Gly Ala

```



		55		60		65		
	GAG CAG CTG AGG GGC CAG ACG TCT GAC AGG CTG GAG ACG GTG ACC CTG							356
	Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val Thr Leu							
		70		75		80		
5	GAT GTT ACC AAG ATG GAG AGC ATC GCT GCA GCT ACT CAG TGG GTG AAG							404
	Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp Val Lys							
		85		90		95		
	GAG CAT GTG GGG GAC AGA GGA CTC TGG GGA CTG GTG AAC AAT GCA GGC							452
	Glu His Val Gly Asp Arg Gly Leu Trp Gly Leu Val Asn Asn Ala Gly							
10		100		105		110		
	ATT CTT ACA CCA ATT ACC TTA TGT GAG TGG CTG AAC ACT GAG GAC TCT							500
	Ile Leu Thr Pro Ile Thr Leu Cys Glu Trp Leu Asn Thr Glu Asp Ser							
		115		120		125		130
	ATG AAT ATG CTC AAA GTG AAC CTC ATT GGT GTG ATC CAG GTG ACC TTG							548
15	Met Asn Met Leu Lys Val Asn Leu Ile Gly Val Ile Gln Val Thr Leu							
		135		140		145		
	AGC ATG CTT CCT TTG GTG AGG AGA GCA CGG GGA AGA ATT GTC AAT GTC							596
	Ser Met Leu Pro Leu Val Arg Arg Ala Arg Gly Arg Ile Val Asn Val							
		150		155		160		
20	TCC AGC ATT CTG GGA AGA GTT GCT TTC TTT GTA GGA GGC TAC TGT GTC							644
	Ser Ser Ile Leu Gly Arg Val Ala Phe Phe Val Gly Gly Tyr Cys Val							
		165		170		175		
	TCC AAG TAT GGA GTG GAA GCC TTT TCA GAT ATT CTG AGG CGT GAG ATT							692
	Ser Lys Tyr Gly Val Glu Ala Phe Ser Asp Ile Leu Arg Arg Glu Ile							
25		180		185		190		
	CAA CAT TTT GGG GTG AAA ATC AGC ATA GTT GAA CCT GGC TAC TTC AGA							740
	Gln His Phe Gly Val Lys Ile Ser Ile Val Glu Pro Gly Tyr Phe Arg							
		195		200		205		210
	ACG GGA ATG ACA AAC ATG ACA CAG TCC TTA GAG CGA ATG AAG CAA AGT							788
30	Thr Gly Met Thr Asn Met Thr Gln Ser Leu Glu Arg Met Lys Gln Ser							
		215		220		225		
	TGG AAA GAA GCC CCC AAG CAT ATT AAG GAG ACC TAT GGA CAG CAG TAT							836
	Trp Lys Glu Ala Pro Lys His Ile Lys Glu Thr Tyr Gly Gln Gln Tyr							
		230		235		240		
35	TTT GAT GCC CTT TAC AAT ATC ATG AAG GAA GGG CTG TTG AAT TGT AGC							884
	Phe Asp Ala Leu Tyr Asn Ile Met Lys Glu Gly Leu Leu Asn Cys Ser							
		245		250		255		
	ACA AAC CTG AAC CTG GTC ACT GAC TGC ATG GAA CAT GCT CTG ACA TCG							932

	Thr	Asn	Leu	Asn	Leu	Val	Thr	Asp	Cys	Met	Glu	His	Ala	Leu	Thr	Ser	
	260						265					270					
	GTG	CAT	CCG	CGA	ACT	CGA	TAT	TCA	GCT	GGC	TGG	GAT	GCT	AAA	TTT	TTC	980
	Val	His	Pro	Arg	Thr	Arg	Tyr	Ser	Ala	Gly	Trp	Asp	Ala	Lys	Phe	Phe	
5	275					280					285				290		
	TTC	ATC	CCT	CTA	TCT	TAT	TTA	CCT	ACA	TCA	CTG	GCA	GAC	TAC	ATT	TTG	1028
	Phe	Ile	Pro	Leu	Ser	Tyr	Leu	Pro	Thr	Ser	Leu	Ala	Asp	Tyr	Ile	Leu	
					295					300					305		
	ACT	AGA	TCT	TGG	CCC	AAA	CCA	GCC	CAG	GCA	GTC	TAAAGAAAAC	TGGGTTGGT				1080
10	Thr	Arg	Ser	Trp	Pro	Lys	Pro	Ala	Gln	Ala	Val						
					310					315							
	GCTTCTTGGA	ATGAAGGCAA	AAATCTGAAA	TTGTTAGTGT	CTCAGTAATC	CTGATTTAGA											1140
	ACCCAGGCTT	TTTGTAACAA	TGTGTTTTCT	TGCCTAAATT	CATTTATCTG	GCATCATCAG											1200
	AGTACTAACA	TGTTTATATT	TCAGATATCC	AAAGCTTACC	ACTTTAGGTG	ATGAATCTTT											1260
15	ACTATTTTAG	CCCTTTTTTG	ATGAGACTAT	TTGTCTAAAG	TGAATCATTT	GTTCTTGCCT											1320
	TATTAAACAG	AGTAGATGGA	AAACAATTT														1349

## (2) INFORMATION FOR SEQ ID NO: 39:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1643
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 25 (ii) SEQUENCE KIND: cDNA to mRNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Homo sapiens*
  - (B) CELL KIND: Liver
  - (D) CLONE NAME: HP01347
- 30
- (ix) SEQUENCE CHARACTERISTICS:
- (A) CHARACTERIZATION CODE: CDS
  - (B) EXISTENCE POSITION: 25.. 915
  - (C) CHARACTERIZATION METHOD: E
- 35
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

	AACATCTGGG GACAGCGGGA AAAC ATG AGT GAC TCC AAG GAA CCA AGG GTG	51
	Met Ser Asp Ser Lys Glu Pro Arg Val	
	1 5	
	CAG CAG CTG GGC CTC CTG GGG TGT CTT GGC CAT GGC GCC CTG GTG CTG	99
5	Gln Gln Leu Gly Leu Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu	
	10 15 20 25	
	CAA CTC CTC TCC TTC ATG CTC TTG GCT GGG GTC CTG GTG GCC ATC CTT	147
	Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu	
	30 35 40	
10	GTC CAA GTG TCC AAG GTC CCC AGC TCC CTA AGT CAG GAA CAA TCC GAG	195
	Val Gln Val Ser Lys Val Pro Ser Ser Leu Ser Gln Glu Gln Ser Glu	
	45 50 55	
	CAA GAC GCA ATC TAC CAG AAC CTG ACC CAG CTT AAA GCT GCA GTG GGT	243
	Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly	
15	60 65 70	
	GAG CTC TCA GAG AAA TCC AAG CTG CAG GAG ATC TAC CAG GAG CTG ACC	291
	Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr	
	75 80 85	
	CAG CTG AAG GCT GCA GTG GGT GAG TTG CCA GAG AAA TCC AAG CTG CAG	339
20	Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln	
	90 95 100 105	
	GAG ATC TAC CAG GAG CTG ACC CGG CTG AAG GCT GCA GTG GGT GAG TTG	387
	Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu	
	110 115 120	
25	CCA GAG AAA TCC AAG CTG CAG GAG ATC TAC CAG GAG CTG ACC CGG CTG	435
	Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu	
	125 130 135	
	AAG GCT GCA GTG GGT GAG TTG CCA GAG AAA TCC AAG CTG CAG GAG ATC	483
	Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile	
30	140 145 150	
	TAC CAG GAG CTG ACC CGG CTG AAG GCT GCA GTG GGT GAG TTG CCA GAG	531
	Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu	
	155 160 165	
	AAA TCC AAG CTG CAG GAG ATC TAC CAG GAG CTG ACG GAG CTG AAG GCT	579
35	Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Glu Leu Lys Ala	
	170 175 180 185	
	GCA GTG GGT GAG TTG CCA GAG AAA TCC AAG CTG CAG GAG ATC TAC CAG	627
	Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln	

		190		195		200		
		GAG CTG ACC CAG CTG AAG GCT GCA GTG GGT GAG TTG CCA GAC CAG TCC	675					
		Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser						
		205		210		215		
5		AAG CAG CAG CAA ATC TAT CAA GAA CTG ACC GAT TTG AAG ACT GCA TTT	723					
		Lys Gln Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe						
		220		225		230		
		GAA CGC CTG TGC CGC CAC TGT CCC AAG GAC TGG ACA TTC TTC CAA GGA	771					
		Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly						
10		235		240		245		
		AAC TGT TAC TTC ATG TCT AAC TCC CAG CGG AAC TGG CAC GAC TCC GTC	819					
		Asn Cys Tyr Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser Val						
		250		255		260		265
		ACC GCC TGC CAG GAA GTG AGG GCC CAG CTC GTC GTA ATC AAA ACT GCT	867					
15		Thr Ala Cys Gln Glu Val Arg Ala Gln Leu Val Val Ile Lys Thr Ala						
		270		275		280		
		GAG GAG CAG CTT CCA GCG GTA CTG GAA CAG TGG AGA ACC CAA CAA	912					
		Glu Glu Gln Leu Pro Ala Val Leu Glu Gln Trp Arg Thr Gln Gln						
		285		290		295		
20		TAGCGGGAAT GAAGACTGTG CGGAATTTAG TGGCAGTGGC TGGAACGACA ATCGATGT	970					
		GACGTTGACA ATTACTGGAT CTGCAAAAAG CCCGCAGCCT GCTTCAGAGA CGAATAGTTG	1030					
		TTTCCCTGCT AGCCTCAGCC TCCATTGTGG TATAGCAGAA CTTACCCAC TTGTAAGCCA	1090					
		GCGCTTCTTC TCTCCATCCT TGGACCTTCA CAAATGCCCT GAGACGGTTC TCTGTTTCGAT	1150					
		TTTTTCATCCC CTATGAACCT GGGTCTTATT CTGTCCTTCT GATGCCTCCA AGTTTCCCTG	1210					
25		GTGTAGAGCT TGTGTTCTTG GCCCATCCTT GGAGCTTTAT AAGTGACCTG AGTGGGATGC	1270					
		ATTTAGGGGG CGGGCTTGGT ATGTTGTATG AATCCACTCT CTGTTCTTTT TGGAGATTAG	1330					
		ACTATTTGGA TTCATGTGTA GCTGCCCTGT CCCCTGGGGC TTTATCTCAT CCATGCAAAC	1390					
		TACCATCTGC TCAACTTCCA GCTACACCCC GTGCACCCTT TTGACTGGGG ACTTGCTGGT	1450					
		TGAAGGAGCT CATCTTGCAG GCTGGAAGCA CCAGGGAATT AATTCCCCCA GTCAACCAAT	1510					
30		GGCATCCAGA GAGGGCATGG AGGCTCCATA CAACCTCTTC CACCCCCACA TCTTTCTTTG	1570					
		TCCTATACAT GTCTTCCATT TGGCTGTTTC TGAGTTGTAG CCTTTATAAT AAAGTGGTAA	1630					
		ATGTTGTAAC TGC	1643					

## 35 (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP01440

10 (ix) SEQUENCE CHARACTERISTICS;

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 38.. 631

(C) CHARACTERIZATION METHOD: E

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

ACTTTCCTC ACCGCCTGTC CTCCTGACA CTCACC ATG TGT ACG GGA AAA TGT 55

Met Cys Thr Gly Lys Cys

1 5

20 GCC CGC TGT GTG GGG CTC TCC CTC ATT ACC CTC TGC CTC GTC TGC ATT 103

Ala Arg Cys Val Gly Leu Ser Leu Ile Thr Leu Cys Leu Val Cys Ile

10                      15                      20

GTG GCC AAC GCC CTC CTG CTG GTA CCT AAT GGG GAG ACC TCC TGG ACC 151

Val Ala Asn Ala Leu Leu Leu Val Pro Asn Gly Glu Thr Ser Trp Thr

25                      25                      30                      35

AAC ACC AAC CAT CTC AGC TTG CAA GTC TGG CTC ATG GGC GGC TTC ATT 199

Asn Thr Asn His Leu Ser Leu Gln Val Trp Leu Met Gly Gly Phe Ile

40                      45                      50

GGC GGG GGC CTA ATG GTA CTG TGT CCG GGG ATT GCA GCC GTT CGG GCA 247

30 Gly Gly Gly Leu Met Val Leu Cys Pro Gly Ile Ala Ala Val Arg Ala

55                      60                      65                      70

GGG GGC AAG GGC TGC TGT GGT GCT GGG TGC TGT GGA AAC CGC TGC AGG 295

Gly Gly Lys Gly Cys Cys Gly Ala Gly Cys Cys Gly Asn Arg Cys Arg

75                      80                      85

35    ATG   CTG   CGC   TCG   GTC   TTC   TCC   TCG   GCG   TTC   GGG   GTG   CTT   GGT   GCC   ATC                      343

Met Leu Arg Ser Val Phe Ser Ser Ala Phe Gly Val Leu Gly Ala Ile

90 95 100

TAC TGC CTC TCG GTG TCT GGA GCT GGG CTC CGA AAT GGA CCC AGA TGC 391

	Tyr	Cys	Leu	Ser	Val	Ser	Gly	Ala	Gly	Leu	Arg	Asn	Gly	Pro	Arg	Cys	
			105					110					115				
	TTA	ATG	AAC	GGC	GAG	TGG	GGC	TAC	CAC	TTC	GAA	GAC	ACC	GCG	GGA	GCT	439
	Leu	Met	Asn	Gly	Glu	Trp	Gly	Tyr	His	Phe	Glu	Asp	Thr	Ala	Gly	Ala	
5		120					125					130					
	TAC	TTG	CTC	AAC	CGC	ACT	CTA	TGG	GAT	CGG	TGC	GAG	GCG	CCC	CCT	CGC	487
	Tyr	Leu	Leu	Asn	Arg	Thr	Leu	Trp	Asp	Arg	Cys	Glu	Ala	Pro	Pro	Arg	
	135				140					145				150			
	GTG	GTC	CCC	TGG	AAT	GTG	ACG	CTC	TTC	TCG	CTG	CTG	GTG	GCC	GCC	TCC	535
10	Val	Val	Pro	Trp	Asn	Val	Thr	Leu	Phe	Ser	Leu	Leu	Val	Ala	Ala	Ser	
				155					160				165				
	TGC	CTG	GAG	ATA	GTA	CTG	TGT	GGG	ATC	CAG	CTG	GTG	AAC	GCG	ACC	ATT	583
	Cys	Leu	Glu	Ile	Val	Leu	Cys	Gly	Ile	Gln	Leu	Val	Asn	Ala	Thr	Ile	
			170				175					180					
15	GGT	GTC	TTC	TGC	GGC	GAT	TGC	AGG	AAA	AAA	CAG	GAC	ACC	CCT	CAC	TG	630
	Gly	Val	Phe	Cys	Gly	Asp	Cys	Arg	Lys	Lys	Gln	Asp	Thr	Pro	His		
		185				190					195						
	AGGCTCCACT	GACCGCCGGG	TTACACCTGC	TCCTTCCTGG	ACGCCTACCT	GGCTCGCTCA											690
	CTCCCTTGCT	CGCTAGAATA	AACTGCTTTG	CGCTCTCTT													729
20																	

## (2) INFORMATION FOR SEQ ID NO: 41:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1322

25 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## 30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP01526

## 35 (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 84.. 749

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

	GAGCCGCAGG TCTGGGCTGC AGTAGGTCCC GGCAACCGCA GGCTCGCGGC GGGCGCTGGG	60
	CGCGGGATCC GACTCTAGTC GTA ATG GAG GCG GGC GGC TTT CTG GAC TCG CTC	113
5	Met Glu Ala Gly Gly Phe Leu Asp Ser Leu	
	1 5 10	
	ATT TAC GGA GCA TGC GTG GTC TTC ACC CTT GGC ATG TTC TCC GCC GGC	161
	Ile Tyr Gly Ala Cys Val Val Phe Thr Leu Gly Met Phe Ser Ala Gly	
	15 20 25	
10	CTC TCG GAC CTC AGG CAC ATG CGA ATG ACC CGG AGT GTG GAC AAC GTC	209
	Leu Ser Asp Leu Arg His Met Arg Met Thr Arg Ser Val Asp Asn Val	
	30 35 40	
	CAG TTC CTG CCC TTT CTC ACC ACG GAA GTC AAC AAC CTG GGC TGG CTG	257
	Gln Phe Leu Pro Phe Leu Thr Thr Glu Val Asn Asn Leu Gly Trp Leu	
15	45 50 55	
	AGT TAT GGG GCT TTG AAG GGA GAC GGG ATC CTC ATC GTC GTC AAC ACA	305
	Ser Tyr Gly Ala Leu Lys Gly Asp Gly Ile Leu Ile Val Val Asn Thr	
	60 65 70	
	GTG GGT GCT GCG CTT CAG ACC CTG TAT ATC TTG GCA TAT CTG CAT TAC	353
20	Val Gly Ala Ala Leu Gln Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr	
	75 80 85 90	
	TGC CCT CGG AAG CGT GTT GTG CTC CTA CAG ACT GCA ACC CTG CTA GGG	401
	Cys Pro Arg Lys Arg Val Val Leu Leu Gln Thr Ala Thr Leu Leu Gly	
	95 100 105	
25	GTC CTT CTC CTG GGT TAT GGC TAC TTT TGG CTC CTG GTA CCC AAC CCT	449
	Val Leu Leu Leu Gly Tyr Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro	
	110 115 120	
	GAG GCC CGG CTT CAG CAG TTG GGC CTC TTC TGC AGT GTC TTC ACC ATC	497
	Glu Ala Arg Leu Gln Gln Leu Gly Leu Phe Cys Ser Val Phe Thr Ile	
30	125 130 135	
	AGC ATG TAC CTC TCA CCA CTG GCT GAC TTG GCT AAG GTG ATT CAA ACT	545
	Ser Met Tyr Leu Ser Pro Leu Ala Asp Leu Ala Lys Val Ile Gln Thr	
	140 145 150	
	AAA TCA ACC CAA TGT CTC TCC TAC CCA CTC ACC ATT GCT ACC CTT CTC	593
35	Lys Ser Thr Gln Cys Leu Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu	
	155 160 165 170	
	ACC TCT GCC TCC TGG TGC CTC TAT GGG TTT CGA CTC AGA GAT CCC TAT	641
	Thr Ser Ala Ser Trp Cys Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr	

130

	175	180	185	
	ATC ATG GTG TCC AAC TTT CCA GGA ATC GTC ACC AGC TTT ATC CGC TTC			689
	Ile Met Val Ser Asn Phe Pro Gly Ile Val Thr Ser Phe Ile Arg Phe			
	190	195	200	
5	TGG CTT TTC TGG AAG TAC CCC CAG GAG CAA GAC AGG AAC TAC TGG CTC			737
	Trp Leu Phe Trp Lys Tyr Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu			
	205	210	215	
	CTG CAA ACC TGAGGCTGCT CATCTGACCA CTGGGCACCT TAGTGCCAAC CTGA			790
	Leu Gln Thr			
10	220			
	ACCAAAGAGA CCTCCTTGTT TCAGCTGGGC CTGCTGTCCA GCTTCCCAGG TGCAGTGGGT			850
	TGTGGGAACA AGAGATGACT TTGAGGATAA AAGGACCAAA GAAAAAGCTT TACTTAGATG			910
	ATTGATTGGG GCCTAGGAGA TGAAATCACT TTTTATTTTT TAGAGATTTT TTTTTTTAAT			970
	TTTGGAGGTT GGGGTGCAAT CTTTAGAATA TGCCTTAAAA GGCCGGGCGC GGTGGCTCAC			1030
15	GCCTGTAATC CCAGCACTTT GGGAGGCCAA GGTGGGCGGA TCGCCTGAGG TCAGGAGTTC			1090
	AAGACCAACC TGACTAACAT GGTGAAACCC CATCTCTACT AAAAATACAA AATTAGCCAG			1150
	GCATGATGGC ACATGCCTGT AATCCCAGAT ACTTGGGAGG CTGAGGCAGG AGAATTGCTT			1210
	GAACCCAGGA GGTGGAGGTT GCAGTGAGCT GAGATCGTGC CATTGTGATA TGAATATGCC			1270
	TTATATGCTG ATATGAATAT GCCTTAAAT AAAGTGTTC CCACCCCTGC CC			1322
20				

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3045
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10230

(ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
- (B) EXISTENCE POSITION: 191.. 946
- (C) CHARACTERIZATION METHOD: E



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

	GTTCGCCTC AGAAGGCTGC CTCGCTGGTC CGAATTCGGT GGCGCCACGT CCGCCCGTCT	60
	CCGCCTTCTG CATCGCGGCT TCGGCGGCTT CCACCTAGAC ACCTAACAGT CGCGGAGCCG	120
5	GCCGCGTCGT GAGGGGGTCG GCACGGGGAG TCGGGCGGTC TTGTGCATCT TGGCTACCTG	180
	TGGGTCTGAAG ATG TCG GAC ATC GGA GAC TGG TTC AGG AGC ATC CCG GCG	229
	Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala	
	1 5 10	
	ATC ACG CGC TAT TGG TTC GCC GCC ACC GTC GCC GTG CCC TTG GTC GGC	277
10	Ile Thr Arg Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly	
	15 20 25	
	AAA CTC GGC CTC ATC AGC CCG GCC TAC CTC TTC CTC TGG CCC GAA GCC	325
	Lys Leu Gly Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala	
	30 35 40 45	
15	TTC CTT TAT CGC TTT CAG ATT TGG AGG CCA ATC ACT GCC ACC TTT TAT	373
	Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr	
	50 55 60	
	TTC CCT GTG GGT CCA GGA ACT GGA TTT CTT TAT TTG GTC AAT TTA TAT	421
	Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr	
20	65 70 75	
	TTC TTA TAT CAG TAT TCT ACG CGA CTT GAA ACA GGA GCT TTT GAT GGG	469
	Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly	
	80 85 90	
	AGG CCA GCA GAC TAT TTA TTC ATG CTC CTC TTT AAC TGG ATT TGC ATC	517
25	Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile	
	95 100 105	
	GTG ATT ACT GGC TTA GCA ATG GAT ATG CAG TTG CTG ATG ATT CCT CTG	565
	Val Ile Thr Gly Leu Ala Met Asp Met Gln Leu Leu Met Ile Pro Leu	
	110 115 120 125	
30	ATC ATG TCA GTA CTT TAT GTC TGG GCC CAG CTG AAC AGA GAC ATG ATT	613
	Ile Met Ser Val Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile	
	130 135 140	
	GTA TCA TTT TGG TTT GGA ACA CGA TTT AAG GCC TGC TAT TTA CCC TGG	661
	Val Ser Phe Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp	
35	145 150 155	
	GTT ATC CTT GGA TTC AAC TAT ATC ATC GGA GGC TCG GTA ATC AAT GAG	709
	Val Ile Leu Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu	
	160 165 170	

	CTT ATT GGA AAT CTG GTT GGA CAT CTT TAT TTT TTC CTA ATG TTC AGA	757
	Leu Ile Gly Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg	
	175 180 185	
	TAC CCA ATG GAC TTG GGA GGA AGA AAT TTT CTA TCC ACA CCT CAG TTT	805
5	Tyr Pro Met Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe	
	190 195 200 205	
	TTG TAC CGC TGG CTG CCC AGT AGG AGA GGA GGA GTA TCA GGA TTT GGT	853
	Leu Tyr Arg Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly	
	210 215 220	
10	GTG CCC CCT GCT AGC ATG AGG CGA GCT GCT GAT CAG AAT GGC GGA GGC	901
	Val Pro Pro Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly	
	225 230 235	
	GGG AGA CAC AAC TGG GGC CAG GGC TTT CGA CTT GGA GAC CAG TGAAGGG	950
	Gly Arg His Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln	
15	240 245 250	
	GCGGCCTCGG GCAGCCGCTC CTCTCAAGCC ACATTTCTCTC CCAGTGCTGG GTGCGCTTAA	1010
	CAACTGCGTT CTGGCTAACA CTGTTGGACC TGACCCACAC TGAATGTAGT CTTTCAGTAC	1070
	GAGACAAAGT TTCTTAAATC CCGAAGAAAA ATATAAGTGT TCCACAAGTT TCACGATTCT	1130
	CATTCAAGTC CTTACTGCTG TGAAGAACAA ATACCAACTG TGCAAATTGC AAAACTGACT	1190
20	ACATTTTTTG GTGTCTTCTC TTCTCCCCTT TCCGTCTGAA TAATGGGTTT TAGCGGGTCC	1250
	TAGTCTGCTG GCATTGAGCT GGGGCTGGGT CACCAAAACC TTCCCAAAG GACCCTTATC	1310
	TCTTTCTTGC ACACATGCCT CTCTCCCACT TTTCCCAACC CCCACATTG CAACTAGAAG	1370
	AGGTTGCCCA TAAATTTGCT CTGCCCTTGA CAGGTTCTGT TATTTATTGA CTTTTGCCAA	1430
	GGCTTGGTCA CAACAATCAT ATTCACGTAA TTTTCCCCTT TTGGTGGCAG AACTGTAGCA	1490
25	ATAGGGGGAG AAGACAAGCA GCGGATGAAG CGTTTTCTCA GCTTTTGGAA TTGCTTCGAC	1550
	CTGACATCCG TTGTAACCGT TTGCCACTTC TTCAGATATT TTTATAAAAA AGTACCACTG	1610
	AGTCAGTGAG GGCCACAGAT TGGTATTAAT GAGATACGAG GGTGTTGCT GGGTGTGTTGT	1670
	TTCCTGAGCT AAGTGATCAA GACTGTAGTG GAGTTGCAGC TAACATGGGT TAGGTTTAAA	1730
	CCGTGGGGGA TGCAACCCCT TTGCGTTTCA TATGTAGGCC TACTGGCTTT GTGTAGCTGG	1790
30	AGTAGTTGGG TTGCTTTGTG TTAGGAGGAT CCAGATCATG TTGGCTACAG GGAGATGCTC	1850
	TCTTTGAGAG GCTCCTGGGC ATTGATTCCA TTTCAATCTC ATTCTGGATA TGTGTTTATT	1910
	GAGTAAAGGA GGAGAGACCC TCATACGCTA TTTAAATGTC ACTTTTTTGC CTATCCCCCG	1970
	TTTTTTGGTC ATGTTTCAAT TAATTGTGAG GAAGGCGCAG CTCCTCTCTG CACGTAGATC	2030
	ATTTTTTAAA GCTAATGTAA GCACATCTAA GGGAATAACA TGATTTAAGG TTGAAATGGC	2090
35	TTTAGAATCA TTTGGGTTTG AGGGTGTGTT ATTTTGAGTC ATGAATGTAC AAGCTCTGTG	2150
	AATCAGACCA GCTTAAATAC CCACACCTTT TTTTCGTAGG TGGGCTTTTC CTATCAGAGC	2210
	TTGGCTCATA ACCAAATAAA GTTTTTTGAA GGCCATGGCT TTTACACAG TTATTTTATT	2270
	TTATGACGTT ATCTGAAAGC AGACTGTTAG GAGCAGTATT GAGTGGCTGT CACACTTTGA	2330

```

GGCAACTAAA AAGGCTTCAA ACGTTTTGAT CAGTTTCTTT TCAGGAAACA TTGTGCTCTA 2390
ACAGTATGAC TATTCTTTCC CCCACTCTTA AACAGTGTGA TGTGTGTTAT CCTAGGAAAT 2450
GAGAGTTGGC AAACAACCTC TCATTTTGAA TAGAGTTTGT GTGTACCTCT CCATATTTAA 2510
TTTATATGAT AAAATAGGTG GGGAGAGTCT GAACCTTAAC TGTCATGTTT TGTTGTTTCA 2570
5 CTGTGGCCAC AATAAAGTTT ACTTGTAATA TTTTAGAGGC CATTACTCCA ATTATGTTGC 2630
ACGTACACTC ATTGTACAGG CGTGGAGACT CATTGTATGT ATAAGAATAT TCTGACAGTG 2690
AGTGACCCCG AGTCTCTGGT GTACCCTCTT ACCAGTCAGC TGCCTGCGAG CAGTCATTTT 2750
TTCCTAAAGG TTTACAAGTA TTTAGAATC TTCAGTTCAG GGCAAAATGT TCATGAAGTT 2810
ATTCTCTTA AACATGGTTA GGAAGCTGAT GACGTTATTG ATTTTGTCTG GATTATGTTT 2870
10 CTGGAATAAT TTTACCAAAA CAAGCTATTT GAGTTTTGAC TTGACAAGGC AAAACATGAC 2930
AGTGGATTCT CTTTACAAAT TGAAAAAAAA AATCCTTATT TTGTATAAAG GACTTCCCTT 2990
TTTGTAAGCT AATCCTTTTT ATTGGTAAAA ATTGTAAATT AAAATGTGCA ACTTG 3045

```

15 (2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- 25 (B) CELL KIND: Epidermoid carcinoma
- (C) CELL LINE: KB
- (D) CLONE NAME: HP10389

(ix) SEQUENCE CHARACTERISTICS:

- 30 (A) CHARACTERIZATION CODE: CDS
- (B) EXISTENCE POSITION: 63.. 383
- (C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

35 ATGACCTTCA CCGGGAGGCT GAGGTCGGAG TCCCGATTTT CTCCTGCTGC TGTGGCCCGG 60
AC ATG GCG ACT CCC GGC CCT GTG ATT CCG GAG GTC CCC TTT GAA CCA 107
Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro

```

	1	5	10	15	
	TCG AAG CCT CCA GTC ATT GAG GGG CTG AGC CCC ACT GTT TAC AGG AAT	155			
	Ser Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn				
	20	25	30		
5	CCA GAG AGT TTC AAG GAA AAG TTC GTT CGC AAG ACC CGC GAG AAC CCG	203			
	Pro Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro				
	35	40	45		
	GTG GTA CCC ATA GGT TGC CTG GCC ACG GCG GCC GCC CTC ACC TAC GGC	251			
	Val Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Ala Leu Thr Tyr Gly				
10	50	55	60		
	CTC TAC TCC TTC CAC CGG GGC AAC AGC CAG CGC TCT CAG CTC ATG ATG	299			
	Leu Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met				
	65	70	75		
	CGC ACC CGG ATC GCC GCC CAG GGT TTC ACG GTC GCA GCC ATC TTG CTG	347			
15	Arg Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu				
	80	85	90	95	
	GGT CTG GCT GTC ACT GCT ATG AAG TCT CGA CCC TAAGCCCAGG GTCTGGCCTT	400			
	Gly Leu Ala Val Thr Ala Met Lys Ser Arg Pro				
	100	105			
20	GAAAGCTCCG CAGAAATGAT TCCAAAACCC AGGGAGCAAC CACTGGCCCT ACCGTGGGAC	460			
	TTACTCCCTC CTCTCCTTTG AGAGGCCCAT GTGTCGCTGG GGAGGAAGTG ACCCTTTGTG	520			
	TAACTGTAAC CGAAAGTTTT TTCAAAAATC CTAGATGCTG TTGTTTGAAT GTTACATACT	580			
	TCTATTTGTG CCACATCTCC CCTCCACTCC CCTGCTTAAT AAACCTCTAAA AATCCACTTG	640			
	TATTTAATTC AGT	653			
25					

## (2) INFORMATION FOR SEQ ID NO: 44:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10408

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 75.. 311

(C) CHARACTERIZATION METHOD: E

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GTAGAAACAG GCCTGTTAAG GAGAGGCCAC CGGGACTTCA GTGTCTCCTC CATCCCAGGA 60  
 GCGCAGTGGC CACT ATG GGG TCT GGG CTG CCC CTT GTC CTC CTC TTG ACC 110  
 10 Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr  
                   1                  5                  10  
 CTC CTT GGC AGC TCA CAT GGA ACA GGG CCG GGT ATG ACT TTG CAA CTG 158  
 Leu Leu Gly Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu  
                   15                  20                  25  
 15 AAG CTG AAG GAG TCT TTT CTG ACA AAT TCC TCC TAT GAG TCC AGC TTC 206  
 Lys Leu Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe  
                   30                  35                  40  
 CTG GAA TTG CTT GAA AAG CTC TGC CTC CTC CTC CAT CTC CCT TCA GGG 254  
 Leu Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly  
 20 45                  50                  55                  60  
 ACC AGC GTC ACC CTC CAC CAT GCA AGA TCT CAA CAC CAT GTT GTC TGC 302  
 Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val Cys  
                   65                  70                  75  
 AAC ACA TGACAGCCAT TGAAGCCTGT GTCCTTCTTG GCCCGGGCTT TTGGGCCGGG GA 360  
 25 Asn Thr  
  
 TGCAGGAGGC AGGCCCCGAC CCTGTCTTTC AGCAGGCCCC CACCCTCCTG AGTGGCAATA 420  
 AATAAAATTC GGTATGCTG 439

30

## (2) INFORMATION FOR SEQ ID NO: 45:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1131

(B) TYPE: Nucleic acid

35

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10412

5

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 56.. 1000  
 (C) CHARACTERIZATION METHOD: E

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

	CTATGAGATC CCGGCCTCAG GGTGGACGCA GTGGTTCTGC ACTGAGGCC C TCGTC ATG	58
		Met
15		1
	GTG GCG CCT GTG TGG TAC TTG GTA GCG GCG GCT CTG CTA GTC GGC TTT	106
	Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly Phe	
	5 10 15	
	ATC CTC TTC CTG ACT CGC AGC CGG GGC CGG GCG GCA TCA GCC GGC CAA	154
20	Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly Gln	
	20 25 30	
	GAG CCA CTG CAC AAT GAG GAG CTG GCA GGA GCA GGC CGG GTG GCC CAG	202
	Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala Gln	
	35 40 45	
25	CCT GGG CCC CTG GAG CCT GAG GAG CCG AGA GCT GGA GGC AGG CCT CGG	250
	Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro Arg	
	50 55 60 65	
	CGC CGG AGG GAC CTG GGC AGC CGC CTA CAG GCC CAG CGT CGA GCC CAG	298
	Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala Gln	
30	70 75 80	
	CGG GTG GCC TGG GCA GAA GCA GAT GAG AAC GAG GAG GAA GCT GTC ATC	346
	Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val Ile	
	85 90 95	
	CTA GCC CAG GAG GAG GAA GGT GTC GAG AAG CCA GCG GAA ACT CAC CTG	394
35	Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His Leu	
	100 105 110	
	TCG GGG AAA ATT GGA GCT AAG AAA CTG CGG AAG CTG GAG GAG AAA CAA	442
	Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Lys Leu Glu Glu Lys Gln	

	115	120	125	
	GCG CGA AAG GCC CAG CGT GAG GCA GAG GAG GCT GAA CGT GAG GAG CGG			490
	Ala Arg Lys Ala Gln Arg Glu Ala Glu Glu Ala Glu Arg Glu Glu Arg			
	130	135	140	145
5	AAA CGA CTC GAG TCC CAG CGC GAA GCT GAG TGG AAG AAG GAG GAG GAG			538
	Lys Arg Leu Glu Ser Gln Arg Glu Ala Glu Trp Lys Lys Glu Glu Glu			
	150	155	160	
	CGG CTT CGC CTG GAG GAG GAG CAG AAG GAG GAG GAG GAG AGG AAG GCC			586
	Arg Leu Arg Leu Glu Glu Glu Gln Lys Glu Glu Glu Glu Arg Lys Ala			
10	165	170	175	
	CGC GAG GAG CAG GCC CAG CGG GAG CAT GAG GAG TAC CTG AAA CTG AAG			634
	Arg Glu Glu Gln Ala Gln Arg Glu His Glu Glu Tyr Leu Lys Leu Lys			
	180	185	190	
	GAG GCC TTT GTG GTG GAG GAG GAA GGC GTA GGA GAG ACC ATG ACT GAG			682
15	Glu Ala Phe Val Val Glu Glu Glu Gly Val Gly Glu Thr Met Thr Glu			
	195	200	205	
	GAA CAG TCC CAG AGC TTC CTG ACA GAG TTC ATC AAC TAC ATC AAG CAG			730
	Glu Gln Ser Gln Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys Gln			
	210	215	220	225
20	TCC AAG GTT GTG CTC TTG GAA GAC CTG GCT TCC CAG GTG GGC CTA CGC			778
	Ser Lys Val Val Leu Leu Glu Asp Leu Ala Ser Gln Val Gly Leu Arg			
	230	235	240	
	ACT CAG GAC ACC ATA AAT CGC ATC CAG GAC CTG CTG GCT GAG GGG ACT			826
	Thr Gln Asp Thr Ile Asn Arg Ile Gln Asp Leu Leu Ala Glu Gly Thr			
25	245	250	255	
	ATA ACA GGT GTG ATT GAC GAC CGG GGC AAG TTC ATC TAC ATA ACC CCA			874
	Ile Thr Gly Val Ile Asp Asp Arg Gly Lys Phe Ile Tyr Ile Thr Pro			
	260	265	270	
	GAG GAA CTG GCC GCC GTG GCC AAC TTC ATC CGA CAG CGG GGC CGG GTG			922
30	Glu Glu Leu Ala Ala Val Ala Asn Phe Ile Arg Gln Arg Gly Arg Val			
	275	280	285	
	TCC ATC GCC GAG CTT GCC CAA GCC AGC AAC TCC CTC ATC GCC TGG GGC			970
	Ser Ile Ala Glu Leu Ala Gln Ala Ser Asn Ser Leu Ile Ala Trp Gly			
	290	295	300	305
35	CGG GAG TCC CCT GCC CAA GCC CCA GCC TGACCCAGT CCTCCCTCT TGG			1020
	Arg Glu Ser Pro Ala Gln Ala Pro Ala			
	310			
	ACTCAGAGTT GGTGTGGCCT ACCTGGCTAT ACATCTTCAT CCCTCCCCAC CATCCTGGGG			1080

AAGTGATGGT GTGGCCAGGC AGTTATAGAT TAAAGGCCTG TGAGTACTGC T

1131

## (2) INFORMATION FOR SEQ ID NO: 46:

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1875  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 10 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10413

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 79.. 666  
 (C) CHARACTERIZATION METHOD: E

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

	CTCGCTCGCT CAGAGGGAGG AGAAAGTGGC GAGTTCCGGA TCCCTGCCTA GCGCGGCCCA	60
25	ACCTTTACTC CAGAGATC ATG GCT GCC GAG GAT GTG GTG GCG ACT GGC GCC	111
	Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala	
	1 5 10	
	GAC CCA AGC GAT CTG GAG AGC GGC GGG CTG CTG CAT GAG ATT TTC ACG	159
	Asp Pro Ser Asp Leu Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr	
30	15 20 25	
	TCG CCG CTC AAC CTG CTG CTG CTT GGC CTC TGC ATC TTC CTG CTC TAC	207
	Ser Pro Leu Asn Leu Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr	
	30 35 40	
	AAG ATC GTG CGC GGC GAC CAG CCG GCG GCC AGC GGC GAC AGC GAC GAC	255
35	Lys Ile Val Arg Gly Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp	
	45 50 55	
	GAC GAG CCG CCC CCT CTG CCC CGC CTC AAG CGG CGC GAC TTC ACC CCC	303
	Asp Glu Pro Pro Pro Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro	



	60	65	70	75	
	GCC GAG CTG CGG CGC TTC GAC GGC GTC CAG GAC CCG CGC ATA CTC ATG				351
	Ala Glu Leu Arg Arg Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met				
		80	85	90	
5	GCC ATC AAC GGC AAG GTG TTC GAT GTG ACC AAA GGC CGC AAA TTC TAC				399
	Ala Ile Asn Gly Lys Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr				
		95	100	105	
	GGG CCC GAG GGC CCG TAT GGG GTC TTT GCT GGA AGA GAT GCA TCC AGG				447
	Gly Pro Glu Gly Pro Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg				
10		110	115	120	
	GGC CTT GCC ACA TTT TGC CTG GAT AAG GAA GCA CTG AAG GAT GAG TAC				495
	Gly Leu Ala Thr Phe Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr				
		125	130	135	
	GAT GAC CTT TCT GAC CTC ACT GCT GCC CAG CAG GAG ACT CTG AGT GAC				543
15	Asp Asp Leu Ser Asp Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp				
		140	145	150	155
	TGG GAG TCT CAG TTC ACT TTC AAG TAT CAT CAC GTG GGC AAA CTG CTG				591
	Trp Glu Ser Gln Phe Thr Phe Lys Tyr His His Val Gly Lys Leu Leu				
		160	165	170	
20	AAG GAG GGG GAG GAG CCC ACT GTG TAC TCA GAT GAG GAA GAA CCA AAA				639
	Lys Glu Gly Glu Glu Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys				
		175	180	185	
	GAT GAG AGT GCC CGG AAA AAT GAT TAAAGCATTG AGTGAAGTA TATCTAT				690
	Asp Glu Ser Ala Arg Lys Asn Asp				
25		190	195		
	TTTTGTATTT TGCAAAATCA TTTGTAACAG TCCACTCTGT CTTTAAAACA TAGTGATTAC				750
	AATATTTAGA AAGTTTTGAG CACTTGCTAT AAGTTTTTTA TAACATCACT AGTGACACTA				810
	ATAAAATTAA CTTCTTAGAA TGCATGATGT GTTTGTGTGT CACAAATCCA GAAAGTGAAC				870
	TGCAGTGCTG TAATACACAT GTTAATACTG TTTTCTTCT ATCTGTAGTT AGTACAGGAT				930
30	GAATTTAAAT GTGTTTTTCC TGAGAGACAA GGAAGACTTG GGTATTTCCC AAAACAGGTA				990
	AAAATCTTAA ATGTGCACCA AGAGCAAAGG ATCAACTTTT AGTCATGATG TTCTGTAAAG				1050
	ACAACAAATC CCTTTTTTTT TCTCAATTGA CTTAAGTCA TGATTTCTGT TTTATCTACC				1110
	TCTAAAGCAA ATCTGCAGTG TTCCAAAGAC TTTGGTATGG ATTAAGCGCT GTCCAGTAAC				1170
	AAAATGAAAT CTCAAAACAG AGCTCAGCTG CAAAAAAGCA TATTTTCTGT GTTTCTGGAC				1230
35	TGCACTGTTG TCCTTGCCCT CACATAGACA CTCAGACACC CTCACAAACA CAGTAGTCTA				1290
	TAGTTAGGAT TAAAATAGGA TCTGAACATT CAAAAGAAAG CTTTGAAAAA AAAGAGCTGG				1350
	CTGGCCTAAA AACCTAAATA TATGATGAAG ATTGTAGGAC TGTCTTCCCA AGCCCCATGT				1410
	TCATGGTGGG GCAATGGTTA TTTGGTTATT TTAAGTCAATT GGTTACTCTC ATTTGAAATG				1470

AGGGAGGGAC ATACAGAATA GGAACAGGTG TTTGCTCTCC TAAGAGCCTT CATGCACACC 1530  
 CCTGAACCAC GAGGAAACAG TACAGTCGCT AGTCAAGTGG TTTTAAAGT AAAGTATATT 1590  
 CATAAGGTAA CAGTTATTCT GTTGTTATAA AACTATACCC ACTGCAAAAG TAGTAGTCAA 1650  
 GTGTCTAGGT CTTTGATATT GCTCTTTTGG TTAACACTAA GCTTAAGTAG ACTATACAGT 1710  
 5 TGTATGAATT TGTAAGAGTA TATGAACACC TAGTGAGATT TCAAACCTGT AATTGTGGTT 1770  
 AAATAGTCAT TGTATTTTCT TGTGAACCTGT GTTTTATGAT TTTACCTCAA ATCAGAAAAC 1830  
 AAAATGATGT GCTTTGGTCA GTTAATAAAA ATGGTTTAC CCACT 1875

10 (2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1563  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 15 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 20 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10415

(ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 25 (B) EXISTENCE POSITION: 72.. 1460  
 (C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

30 AAATTGGGCC AGGCTGAGGC GCTGCTGCTG GAGCGGCCGA TCCGAGACGT GGCTCCCTGG 60  
 GCGGCAGAAC C ATG TTG GAC TTC GCG ATC TTC GCC GTT ACC TTC TTG CTG 110  
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu  
 1 5 10  
 GCG TTG GTG GGA GCC GTG CTC TAC CTC TAT CCG GCT TCC AGA CAA GCT 158  
 35 Ala Leu Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala  
 15 20 25  
 GCA GGA ATT CCA GGG ATT ACT CCA ACT GAA GAA AAA GAT GGT AAT CTT 206  
 Ala Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu

	30		35		40		45										
	CCA	GAT	ATT	GTG	AAT	AGT	GGA	AGT	TTG	CAT	GAG	TTC	CTG	GTT	AAT	TTG	254
	Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn	Leu	
				50					55						60		
5	CAT	GAG	AGA	TAT	GGG	CCT	GTG	GTC	TCC	TTC	TGG	TTT	GGC	AGG	CGC	CTC	302
	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg	Arg	Leu	
				65					70						75		
	GTG	GTT	AGT	TTG	GGC	ACT	GTT	GAT	GTA	CTG	AAG	CAG	CAT	ATC	AAT	CCC	350
	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His	Ile	Asn	Pro	
10			80						85						90		
	AAT	AAG	ACA	TTG	GAC	CCT	TTT	GAA	ACC	ATG	CTG	AAG	TCA	TTA	TTA	AGG	398
	Asn	Lys	Thr	Leu	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys	Ser	Leu	Leu	Arg	
			95						100						105		
	TAT	CAA	TCT	GGT	GGT	GGC	AGT	GTG	AGT	GAA	AAC	CAC	ATG	AGG	AAA	AAA	446
15	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn	His	Met	Arg	Lys	Lys	
				110					115						120		
	TTG	TAT	GAA	AAT	GGT	GTG	ACT	GAT	TCT	CTG	AAG	AGT	AAC	TTT	GCC	CTC	494
	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu	Lys	Ser	Asn	Phe	Ala	Leu	
				130						135					140		
20	CTC	CTA	AAG	CTT	TCA	GAA	GAA	TTA	TTA	GAT	AAA	TGG	CTC	TCC	TAC	CCA	542
	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu	Asp	Lys	Trp	Leu	Ser	Tyr	Pro	
				145						150					155		
	GAG	ACC	CAG	CAC	GTG	CCC	CTC	AGC	CAG	CAT	ATG	CTT	GGT	TTT	GCT	ATG	590
	Glu	Thr	Gln	His	Val	Pro	Leu	Ser	Gln	His	Met	Leu	Gly	Phe	Ala	Met	
25			160						165						170		
	AAG	TCT	GTT	ACA	CAG	ATG	GTA	ATG	GGT	AGT	ACA	TTT	GAA	GAT	GAT	CAG	638
	Lys	Ser	Val	Thr	Gln	Met	Val	Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	
			175						180						185		
	GAA	GTC	ATT	CGC	TTC	CAG	AAG	AAT	CAT	GGC	ACA	GTT	TGG	TCT	GAG	ATT	686
30	Glu	Val	Ile	Arg	Phe	Gln	Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	
				190					195						200		
	GGA	AAA	GGC	TTT	CTA	GAT	GGG	TCA	CTT	GAT	AAA	AAC	ATG	ACT	CGG	AAA	734
	Gly	Lys	Gly	Phe	Leu	Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	
				210						215					220		
35	AAA	CAA	TAT	GAA	GAT	GCC	CTC	ATG	CAA	CTG	GAG	TCT	GTT	TTA	AGG	AAC	782
	Lys	Gln	Tyr	Glu	Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	
				225						230					235		
	ATC	ATA	AAA	GAA	CGA	AAA	GGA	AGG	AAC	TTC	AGT	CAA	CAT	ATT	TTC	ATT	830

	Ile	Ile	Lys	Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	
			240					245					250				
	GAC	TCC	TTA	GTA	CAA	GGG	AAC	CTT	AAT	GAC	CAA	CAG	ATC	CTA	GAA	GAC	878
	Asp	Ser	Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	
5			255					260					265				
	AGT	ATG	ATA	TTT	TCT	CTG	GCC	AGT	TGC	ATA	ATA	ACT	GCA	AAA	TTG	TGT	926
	Ser	Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys	
	270						275					280				285	
	ACC	TGG	GCA	ATC	TGT	TTT	TTA	ACC	ACC	TCT	GAA	GAA	GTT	CAA	AAA	AAA	974
10	Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	Lys	
					290					295					300		
	TTA	TAT	GAA	GAG	ATA	AAC	CAA	GTT	TTT	GGA	AAT	GGT	CCT	GTT	ACT	CCA	1022
	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	Thr	Pro	
					305					310					315		
15	GAG	AAA	ATT	GAG	CAG	CTC	AGA	TAT	TGT	CAG	CAT	GTG	CTT	TGT	GAA	ACT	1070
	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	Cys	Glu	Thr	
					320					325					330		
	GTT	CGA	ACT	GCC	AAA	CTG	ACT	CCA	GTT	TCT	GCC	CAG	CTT	CAA	GAT	ATT	1118
	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	Leu	Gln	Asp	Ile	
20			335					340					345				
	GAA	GGA	AAA	ATT	GAC	CGA	TTT	ATT	ATT	CCT	AGA	GAG	ACC	CTC	GTC	CTT	1166
	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	Glu	Thr	Leu	Val	Leu	
	350						355					360				365	
	TAT	GCC	CTT	GGT	GTG	GTA	CTT	CAG	GAT	CCT	AAT	ACT	TGG	CCA	TCT	CCA	1214
25	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	Asn	Thr	Trp	Pro	Ser	Pro	
					370					375					380		
	CAC	AAG	TTT	GAT	CCA	GAT	CGG	TTT	GAT	GAT	GAA	TTA	GTA	ATG	AAA	ACT	1262
	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	Asp	Glu	Leu	Val	Met	Lys	Thr	
					385					390					395		
30	TTT	TCC	TCA	CTT	GGA	TTC	TCA	GGC	ACA	CAG	GAG	TGT	CCA	GAG	TTG	AGG	1310
	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	
					400					405					410		
	TTT	GCA	TAT	ATG	GTG	ACC	ACA	GTA	CTT	CTT	AGT	GTA	TTG	GTG	AAG	AGA	1358
	Phe	Ala	Tyr	Met	Val	Thr	Thr	Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	
35			415					420					425				
	CTG	CAC	CTA	CTT	TCT	GTG	GAG	GGA	CAG	GTT	ATT	GAA	ACA	AAG	TAT	GAA	1406
	Leu	His	Leu	Leu	Ser	Val	Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	
	430						435					440				445	

5 Tyr

TTAAAAAAAA TCTATGTTGA ATCCTTTTAT AAACCAGTAT CACTTTGTAA TAT 1563

10 (2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2030

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

15 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

20 (B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10419

(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

25 (B) EXISTENCE POSITION: 171.. 914

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

30 CATTGGGGT TTCGGTCCC CCCCTTCCCC TTCCCCGGGG TCTGGGGGTG ACATTGCACC 60

GCGCCCCTCG TGGGGTCGCG TTGCCACCCC ACGCGGACTC CCCAGCTGGC GCGCCCCTCC 120

CATTTGCCTG TCCTGGTCAG GCCCCACCC CCCTTCCCAC CTGACCAGCC ATG GGG 176

Met Gly

1

35 GCT GCG GTG TTT TTC GGC TGC ACT TTC GTC GCG TTC GGC CCG GCC TTC 224

Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro Ala Phe

5

10

15

GCG CTT TTC TTG ATC ACT GTG GCT GGG GAC CCG CTT CGC GTT ATC ATC 272

	Ala	Leu	Phe	Leu	Ile	Thr	Val	Ala	Gly	Asp	Pro	Leu	Arg	Val	Ile	Ile	
	20						25					30					
	CTG	GTC	GCA	GGG	GCA	TTT	TTC	TGG	CTG	GTC	TCC	CTG	CTC	CTG	GCC	TCT	320
	Leu	Val	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	Leu	Leu	Leu	Ala	Ser	
5	35					40					45					50	
	GTG	GTC	TGG	TTC	ATC	TTG	GTC	CAT	GTG	ACC	GAC	CGG	TCA	GAT	GCC	CGG	368
	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr	Asp	Arg	Ser	Asp	Ala	Arg	
					55					60					65		
	CTC	CAG	TAC	GGC	CTC	CTG	ATT	TTT	GGT	GCT	GCT	GTC	TCT	GTC	CTT	CTA	416
10	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly	Ala	Ala	Val	Ser	Val	Leu	Leu	
				70					75						80		
	CAG	GAG	GTG	TTC	CGC	TTT	GCC	TAC	TAC	AAG	CTG	CTT	AAG	AAG	GCA	GAT	464
	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Asp	
				85				90							95		
15	GAG	GGG	TTA	GCA	TCG	CTG	AGT	GAG	GAC	GGA	AGA	TCA	CCC	ATC	TCC	ATC	512
	Glu	Gly	Leu	Ala	Ser	Leu	Ser	Glu	Asp	Gly	Arg	Ser	Pro	Ile	Ser	Ile	
		100					105					110					
	CGC	CAG	ATG	GCC	TAT	GTT	TCT	GGT	CTC	TCC	TTC	GGT	ATC	ATC	AGT	GGT	560
	Arg	Gln	Met	Ala	Tyr	Val	Ser	Gly	Leu	Ser	Phe	Gly	Ile	Ile	Ser	Gly	
20	115					120					125					130	
	GTC	TTC	TCT	GTT	ATC	AAT	ATT	TTG	GCT	GAT	GCA	CTT	GGG	CCA	GGT	GTG	608
	Val	Phe	Ser	Val	Ile	Asn	Ile	Leu	Ala	Asp	Ala	Leu	Gly	Pro	Gly	Val	
					135					140					145		
	GTT	GGG	ATC	CAT	GGA	GAC	TCA	CCC	TAT	TAC	TTC	CTG	ACT	TCA	GCC	TTT	656
25	Val	Gly	Ile	His	Gly	Asp	Ser	Pro	Tyr	Tyr	Phe	Leu	Thr	Ser	Ala	Phe	
				150						155					160		
	CTG	ACA	GCA	GCC	ATT	ATC	CTG	CTC	CAT	ACC	TTT	TGG	GGA	GTT	GTG	TTC	704
	Leu	Thr	Ala	Ala	Ile	Ile	Leu	Leu	His	Thr	Phe	Trp	Gly	Val	Val	Phe	
				165				170				175					
30	TTT	GAT	GCC	TGT	GAG	AGG	AGA	CGG	TAC	TGG	GCT	TTG	GGC	CTG	GTG	GTT	752
	Phe	Asp	Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	Ala	Leu	Gly	Leu	Val	Val	
		180					185					190					
	GGG	AGT	CAC	CTA	CTG	ACA	TCG	GGA	CTG	ACA	TTC	CTG	AAC	CCC	TGG	TAT	800
	Gly	Ser	His	Leu	Leu	Thr	Ser	Gly	Leu	Thr	Phe	Leu	Asn	Pro	Trp	Tyr	
35	195					200					205					210	
	GAG	GCC	AGC	CTG	CTG	CCC	ATC	TAT	GCA	GTC	ACT	GTT	TCC	ATG	GGG	CTC	848
	Glu	Ala	Ser	Leu	Leu	Pro	Ile	Tyr	Ala	Val	Thr	Val	Ser	Met	Gly	Leu	
					215						220					225	

TGG GCC TTC ATC ACA GCT GGA GGG TCC CTC CGA AGT ATT CAG CGC AGC 896  
 Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln Arg Ser  
 230 235 240  
 CTC TTG TGT AAG GAC TGA CTACCTG GACTGATCGC CTGACAGATC CCACCTGCC 950  
 5 Leu Leu Cys Lys Asp  
 245  
 TGTCCACTGC CCATGACTGA GCCCAGCCCC AGCCCGGGTC CATTGCCCAC ATTCTCTGTC 1010  
 TCCTTCTCGT CGGTCTACCC CACTACCTCC AGGGTTTTGC TTTGTCCTTT TGTGACCGTT 1070  
 AGTCTCTAAG CTTTACCAGG AGCAGCCTGG GTTCAGCCAG TCAGTGA CTG GTGGGTTTGA 1130  
 10 ATCTGCACTT ATCCCCACCA CCTGGGGACC CCCTTGTTGT GTCCAGGACT CCCCTGTGT 1190  
 CAGTGCTCTG CTCTCACCTT GCCCAAGACT CACCTCCCTT CCCCTCTGCA GGCCGACGGC 1250  
 AGGAGGACAG TCGGGTGATG GTGTATTCTG CCCTGCGCAT CCCACCCGAG GACTGAGGGA 1310  
 ACCTAGGGGG GACCCCTGGG CCTGGGGTGC CCTCCTGATG TCCTCGCCCT GTATTTCTCC 1370  
 ATCTCCAGTT CTGGACAGTG CAGGTTGCCA AGAAAAGGGA CCTAGTTTAG CCATTGCCCT 1430  
 15 GGAGATGAAA TTAATGGAGG CTCAAGGATA GATGAGCTCT GAGTTTCTCA GTACTCCCTC 1490  
 AAGACTGGAC ATCTTGGTCT TTTTCTCAGG CCTGAGGGGG AACCATTTTT GGTGTGATAA 1550  
 ATACCCTAAA CTGCCTTTTT TTCTTTTTTG AGGTGGGGGG AGGGAGGAGG TATATTGGAA 1610  
 CTCTTCTAAC CTCCTTGGGC TATATTTTCT CTCCTCGAGT TGCTCCTCAT GGCTGGGCTC 1670  
 ATTTGCGTCC CTTTCTCCTT GGTCCCAGAC CTTGGGGGAA AGGAAGGAAG TGCATGTTTG 1730  
 20 GGAAGTGGCA TTAAGTGAAC TAATGGTTTT AACCTCCTTA ACCACCAGCA TCCCTCCTCT 1790  
 CCCCAAGGTG AAGTGGAGGG TGCTGTGGTG AGCTGGCCAC TCCAGAGCTG CAGTGCCACT 1850  
 GGAGGAGTCA GACTACCATG ACATCGTAGG GAAGGAGGGG AGATTTTTTT GTAGTTTTTA 1910  
 ATTGGGGTGT GGGAGGGGCG GGGAGGTTTT CTATAAACTG TATCATTTTC TGCTGAGGGT 1970  
 GGAGTGTCCTC ATCCTTTTAA TCAAGGTGAT TGTGATTTTG ACTAATAAAA AAGAATTTGT 2030  
 25

## (2) INFORMATION FOR SEQ ID NO: 49:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## 35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10424

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 98.. 439

(C) CHARACTERIZATION METHOD: E

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

AAAGTTTCCC AAATCCAGGC GGCTAGAGGC CCACTGCTTC CCAACTACCA GCTGAGGGGG 60  
 TCCGTCCCGA GAAGGGAGAA GAGGCCGAAG AGGAAAC ATG AAC TTC TAT TTA CTC 115  
 10 Met Asn Phe Tyr Leu Leu  
 1 5  
 CTA GCG AGC AGC ATT CTG TGT GCC TTG ATT GTC TTC TGG AAA TAT CGC 163  
 Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile Val Phe Trp Lys Tyr Arg  
 10 15 20  
 15 CGC TTT CAG AGA AAC ACT GGC GAA ATG TCA TCA AAT TCA ACT GCT CTT 211  
 Arg Phe Gln Arg Asn Thr Gly Glu Met Ser Ser Asn Ser Thr Ala Leu  
 25 30 35  
 GCA CTA GTG AGA CCC TCT TCT TCT GGG TTA ATT AAC AGC AAT ACA GAC 259  
 Ala Leu Val Arg Pro Ser Ser Ser Gly Leu Ile Asn Ser Asn Thr Asp  
 20 40 45 50  
 AAC AAT CTT GCA GTC TAC GAC CTC TCT CGG GAT ATT TTA AAT AAT TTC 307  
 Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg Asp Ile Leu Asn Asn Phe  
 55 60 65 70  
 CCA CAC TCA ATA GCC AGG CAG AAG CGA ATA TTG GTA AAC CTC AGT ATG 355  
 25 Pro His Ser Ile Ala Arg Gln Lys Arg Ile Leu Val Asn Leu Ser Met  
 75 80 85  
 GTG GAA AAC AAG CTG GTT GAA CTG GAA CAT ACT CTA CTT AGC AAG GGT 403  
 Val Glu Asn Lys Leu Val Glu Leu Glu His Thr Leu Leu Ser Lys Gly  
 90 95 100  
 30 TTC AGA GGT GCA TCA CCT CAC CGG AAA TCC ACC TAAAAGCGTA CAGG 450  
 Phe Arg Gly Ala Ser Pro His Arg Lys Ser Thr  
 105 110  
 ATGTAATGCC AGTGGTGGAA ATCATTAAAG ACACCTTGA GTAG 493

35

## (2) INFORMATION FOR SEQ ID NO: 50:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2044



(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Epidermoid carcinoma

(C) CELL LINE: KB

10

(D) CLONE NAME: HP10428

(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 288.. 1385

15

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

	AGATTCCGGC CTGGAGCTCC CAGGGCCGAG CAGACCTTGG GACCTGTGAG CGCTGCATCC	60
20	AATTAACCAT GGGAAGGGTC AGCACCAGCC ACCAGCCCCT TAGGTGAGGA CTCTGCCTGG	120
	GGCTCTGCTG ATGGTTCCGA ATCATGGAGC TGCAGAGAGC TCCTCCAGCC TGGAGACGTT	180
	CTTGGTGAAA GCTGTGGTCT AACTCCACCG GCTCTTCCTG CACATTGTAT TCAAGAGGGG	240
	TGCCTGCCCC CGCTGACTCA GGAGCTCCGG TGCTGCAGCC GCCACGA ATG GGG AGG	296
		Met Gly Arg
25		1
	TGG GCC CTC GAT GTG GCC TTT TTG TGG AAG GCG GTG TTG ACC CTG GGG	344
	Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu Thr Leu Gly	
	5 10 15	
	CTG GTG CTT CTC TAC TAC TGC TTC TCC ATC GGC ATC ACC TTC TAC AAC	392
30	Leu Val Leu Leu Tyr Tyr Cys Phe Ser Ile Gly Ile Thr Phe Tyr Asn	
	20 25 30 35	
	AAG TGG CTG ACA AAG AGC TTC CAT TTC CCC CTC TTC ATG ACG ATG CTG	440
	Lys Trp Leu Thr Lys Ser Phe His Phe Pro Leu Phe Met Thr Met Leu	
	40 45 50	
35	CAC CTG GCC GTG ATC TTC CTC TTC TCC GCC CTG TCC AGG GCG CTG GTT	488
	His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser Arg Ala Leu Val	
	55 60 65	
	CAG TGC TCC AGC CAC AGG GCC CGT GTG GTG CTG AGC TGG GCC GAC TAC	536

	Gln	Cys	Ser	Ser	His	Arg	Ala	Arg	Val	Val	Leu	Ser	Trp	Ala	Asp	Tyr	
			70					75					80				
	CTC	AGA	AGA	GTG	GCT	CCC	ACA	GCT	CTG	GCG	ACG	GCG	CTT	GAC	GTG	GGC	584
	Leu	Arg	Arg	Val	Ala	Pro	Thr	Ala	Leu	Ala	Thr	Ala	Leu	Asp	Val	Gly	
5		85					90					95					
	TTG	TCC	AAC	TGG	AGC	TTC	CTG	TAT	GTC	ACC	GTC	TCG	CTG	TAC	ACA	ATG	632
	Leu	Ser	Asn	Trp	Ser	Phe	Leu	Tyr	Val	Thr	Val	Ser	Leu	Tyr	Thr	Met	
	100					105					110				115		
	ACC	AAA	TCC	TCA	GCT	GTC	CTC	TTC	ATC	TTG	ATC	TTC	TCT	CTG	ATC	TTC	680
10	Thr	Lys	Ser	Ser	Ala	Val	Leu	Phe	Ile	Leu	Ile	Phe	Ser	Leu	Ile	Phe	
					120					125				130			
	AAG	CTG	GAG	GAG	CTG	CGC	GCG	GCA	CTG	GTC	CTG	GTG	GTC	CTC	CTC	ATC	728
	Lys	Leu	Glu	Glu	Leu	Arg	Ala	Ala	Leu	Val	Leu	Val	Val	Leu	Leu	Ile	
					135				140					145			
15	GCC	GGG	GGT	CTC	TTC	ATG	TTC	ACC	TAC	AAG	TCC	ACA	CAG	TTC	AAC	GTG	776
	Ala	Gly	Gly	Leu	Phe	Met	Phe	Thr	Tyr	Lys	Ser	Thr	Gln	Phe	Asn	Val	
					150				155					160			
	GAG	GGC	TTC	GCC	TTG	GTG	CTG	GGG	GCC	TCG	TTC	ATC	GGT	GGC	ATT	CGC	824
	Glu	Gly	Phe	Ala	Leu	Val	Leu	Gly	Ala	Ser	Phe	Ile	Gly	Gly	Ile	Arg	
20		165					170				175						
	TGG	ACC	CTC	ACC	CAG	ATG	CTC	CTG	CAG	AAG	GCT	GAA	CTC	GGC	CTC	CAG	872
	Trp	Thr	Leu	Thr	Gln	Met	Leu	Leu	Gln	Lys	Ala	Glu	Leu	Gly	Leu	Gln	
	180				185					190				195			
	AAT	CCC	ATC	GAC	ACC	ATG	TTC	CAC	CTG	CAG	CCA	CTC	ATG	TTC	CTG	GGG	920
25	Asn	Pro	Ile	Asp	Thr	Met	Phe	His	Leu	Gln	Pro	Leu	Met	Phe	Leu	Gly	
					200					205				210			
	CTC	TTC	CCT	CTC	TTT	GCT	GTA	TTT	GAA	GGT	CTC	CAT	TTG	TCC	ACA	TCT	968
	Leu	Phe	Pro	Leu	Phe	Ala	Val	Phe	Glu	Gly	Leu	His	Leu	Ser	Thr	Ser	
					215				220					225			
30	GAG	AAA	ATC	TTC	CGT	TTC	CAG	GAC	ACA	GGG	CTG	CTC	CTG	CGG	GTA	CTT	1016
	Glu	Lys	Ile	Phe	Arg	Phe	Gln	Asp	Thr	Gly	Leu	Leu	Leu	Arg	Val	Leu	
					230				235					240			
	GGG	AGC	CTC	TTC	CTT	GGC	GGG	ATT	CTC	GCC	TTT	GGT	TTG	GGC	TTC	TCT	1064
	Gly	Ser	Leu	Phe	Leu	Gly	Gly	Ile	Leu	Ala	Phe	Gly	Leu	Gly	Phe	Ser	
35		245					250					255					
	GAG	TTC	CTC	CTG	GTC	TCC	AGA	ACC	TCC	AGC	CTC	ACT	CTC	TCC	ATT	GCC	1112
	Glu	Phe	Leu	Leu	Val	Ser	Arg	Thr	Ser	Ser	Leu	Thr	Leu	Ser	Ile	Ala	
	260					265					270				275		

	GGC ATT TTT AAG GAA GTC TGC ACT TTG CTG TTG GCA GCT CAT CTG CTG	1160
	Gly Ile Phe Lys Glu Val Cys Thr Leu Leu Leu Ala Ala His Leu Leu	
	280 285 290	
	GGC GAT CAG ATC AGC CTC CTG AAC TGG CTG GGC TTC GCC CTC TGC CTC	1208
5	Gly Asp Gln Ile Ser Leu Leu Asn Trp Leu Gly Phe Ala Leu Cys Leu	
	295 300 305	
	TCG GGA ATA TCC CTC CAC GTT GCC CTC AAA GCC CTG CAT TCC AGA GGT	1256
	Ser Gly Ile Ser Leu His Val Ala Leu Lys Ala Leu His Ser Arg Gly	
	310 315 320	
10	GAT GGT GGC CCC AAG GCC TTG AAG GGG CTG GGC TCC AGC CCC GAC CTG	1304
	Asp Gly Gly Pro Lys Ala Leu Lys Gly Leu Gly Ser Ser Pro Asp Leu	
	325 330 335	
	GAG CTG CTG CTC CGG AGC AGC CAG CGG GAG GAA GGT GAC AAT GAG GAG	1352
	Glu Leu Leu Leu Arg Ser Ser Gln Arg Glu Glu Gly Asp Asn Glu Glu	
15	340 345 350 355	
	GAG GAG TAC TTT GTG GCC CAG GGG CAG CAG TGACCAGCCA GGGCAAAT	1400
	Glu Glu Tyr Phe Val Ala Gln Gly Gln Gln	
	360 365	
	GGCTTAGAAG CAGGCCACTC CCCAGCCTGC TGCCAGCACT CACTGTGCTC AAGCCGCCAG	1460
20	GGCTCATCAT GGTAGCTGGG AGCTGTGGAC GGGAGTCACC AGGTGGTGGG GCCAAGCCAG	1520
	GGACTCATGA CTTTTGCCCC TCCCTTCAGA GCCTGGTCAC ACAAGGGGCG AGCACCAGGC	1580
	CAGCCTGGGA CTGGCCAGAG CTGGGCCCAA GCTGCGCTGG AATCGCAGCA GGAGAGGGGA	1640
	GTGGGCTGGT TCTTCCCACC ACTTCCCAGG CTCTGACAGC CGAGACTCAT TTCCAAGGCA	1700
	CAGCAGCTTT CTAAAGGGAC TGAGTTTGA CTGGGTTTTG GACCTCCAGG GGCTGGAGCT	1760
25	TCATCACCTG GGCAGTGTCT TTTCTCAGAG AGCAGGTTTC TTTATAGTTT GGAAATAAAT	1820
	GGTTCACGGT CCACTGGCCG CCTTGTGTTG CTGGAGACGT GGGGGCAGG AGGGGACAGT	1880
	GTGGGCCTGG CCTCTCCTTT CCTTTCCTG CCTGGAGCCT TCTTCAAATG TCTGGTCTTA	1940
	AGCCAGGCCT CCTTCATTTT CTCGCTCCTG TTAGAACACC AGTCCCCTCC CCAGTGGGGC	2000
	CCCACTGCAC CTGCTGGCAG GAAATAAATG AATGTTTACT GAGT	2044
30		

## (2) INFORMATION FOR SEQ ID NO: 51:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1043

35

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10429

5

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 157.. 837  
 (C) CHARACTERIZATION METHOD: E

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

	ATTAGCATAA CCCTTCCTCA GGAAGAGTGA GATTTTATAT TTGACAATAA AGTGTTAGAC	60
	TCCATTTCTA AATACCAGAC TTCAAAAGAT AAGGTTCAAA AGTGTTATAA GAAGATATTC	120
15	CTTTTTTTGT CCTAGAGAAC TTATTTTCCT GTGAAA ATG CCT ACC ACA AAG AAG	174
	Met Pro Thr Thr Lys Lys	
	1 5	
	ACA TTG ATG TTC TTA TCA AGC TTT TTC ACC AGC CTT GGG TCC TTC ATT	222
	Thr Leu Met Phe Leu Ser Ser Phe Phe Thr Ser Leu Gly Ser Phe Ile	
20	10 15 20	
	GTA ATT TGC TCT ATT CTT GGG ACA CAA GCA TGG ATC ACC AGT ACA ATT	270
	Val Ile Cys Ser Ile Leu Gly Thr Gln Ala Trp Ile Thr Ser Thr Ile	
	25 30 35	
	GCT GTT AGA GAC TCT GCT TCA AAT GGG AGC ATT TTC ATC ACT TAC GGA	318
25	Ala Val Arg Asp Ser Ala Ser Asn Gly Ser Ile Phe Ile Thr Tyr Gly	
	40 45 50	
	CTT TTT CGT GGG GAG AGT AGT GAA GAA TTG AGT CAC GGA CTT GCA GAA	366
	Leu Phe Arg Gly Glu Ser Ser Glu Glu Leu Ser His Gly Leu Ala Glu	
	55 60 65 70	
30	CCA AAG AAA AAG TTT GCA GTT TTA GAG ATA CTG AAT AAT TCT TCC CAA	414
	Pro Lys Lys Lys Phe Ala Val Leu Glu Ile Leu Asn Asn Ser Ser Gln	
	75 80 85	
	AAA ACT CTG CAT TCG GTG ACT ATC CTG TTC CTG GTC CTG AGT TTG ATC	462
	Lys Thr Leu His Ser Val Thr Ile Leu Phe Leu Val Leu Ser Leu Ile	
35	90 95 100	
	ACG TCG CTG CTG AGC TCT GGG TTT ACC TTC TAC AAC AGC ATC AGC AAC	510
	Thr Ser Leu Leu Ser Ser Gly Phe Thr Phe Tyr Asn Ser Ile Ser Asn	
	105 110 115	

	CCT TAC CAG ACA TTC CTG GGG CCG ACG GGG GTG TAC ACC TGG AAC GGG	558
	Pro Tyr Gln Thr Phe Leu Gly Pro Thr Gly Val Tyr Thr Trp Asn Gly	
	120 125 130	
	CTC GGT GCA TCC TTC GTT TTT GTG ACC ATG ATA CTG TTT GTG GCG AAC	606
5	Leu Gly Ala Ser Phe Val Phe Val Thr Met Ile Leu Phe Val Ala Asn	
	135 140 145 150	
	ACG CAG TCC AAC CAA CTC TCC GAA GAG TTG TTC CAA ATG CTT TAC CCG	654
	Thr Gln Ser Asn Gln Leu Ser Glu Glu Leu Phe Gln Met Leu Tyr Pro	
	155 160 165	
10	GCA ACC ACC AGT AAA GGA ACG ACC CAC AGT TAC GGA TAC TCG TTC TGG	702
	Ala Thr Thr Ser Lys Gly Thr Thr His Ser Tyr Gly Tyr Ser Phe Trp	
	170 175 180	
	CTC ATA CTG CTC GTC ATT CTT CTA AAT ATA GTC ACT GTA ACC ATC ATC	750
	Leu Ile Leu Leu Val Ile Leu Leu Asn Ile Val Thr Val Thr Ile Ile	
15	185 190 195	
	ATT TTC TAC CAG AAG GCC AGA TAC CAG CGG AAG CAG GAG CAG AGA AAG	798
	Ile Phe Tyr Gln Lys Ala Arg Tyr Gln Arg Lys Gln Glu Gln Arg Lys	
	200 205 210	
	CCA ATG GAA TAT GCT CCA AGG GAC GGA ATT TTA TTC TGAATTCTCT TTCATC	850
20	Pro Met Glu Tyr Ala Pro Arg Asp Gly Ile Leu Phe	
	215 220 225	
	TCATTTTGGC GTTGCATCTA TTGTACATCA GCCCTGAGTA GTAACCTGGTT AGCTTCTCTG	910
	GACAATTCAG CATGGTAACG TGA CTGTGACAGC ATTTGTGTTT CATGACACTG	970
	TGTTCTTCAT TGATGCTGTA CTCCTGAAAA TTTTTCAC AAGGTTGGGG AAATGAATGG	1030
25	GAAATGTCGC TGG	1043

## (2) INFORMATION FOR SEQ ID NO: 52:

## (i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 972

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

35

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP10432

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 5 (B) EXISTENCE POSITION: 29.. 418  
 (C) CHARACTERIZATION METHOD: E

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

10  AGACAGCGGC GGGCGCAGGA CGTGCACT ATG GCT CGG GGC TCG CTG CGC CGG      52
      Met Ala Arg Gly Ser Leu Arg Arg
          1              5
      TTG CTG CGG CTC CTC GTG CTG GGG CTC TGG CTG GCG TTG CTG CGC TCC      100
      Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser
15      10              15              20
      GTG GCC GGG GAG CAA GCG CCA GGC ACC GCC CCC TGC TCC CGC GGC AGC      148
      Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser
      25              30              35              40
      TCC TGG AGC GCG GAC CTG GAC AAG TGC ATG GAC TGC GCG TCT TGC AGG      196
20  Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg
      45              50              55
      GCG CGA CCG CAC AGC GAC TTC TGC CTG GGC TGC GCT GCA GCA CCT CCT      244
      Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro
      60              65              70
25  GCC CCC TTC CGG CTG CTT TGG CCC ATC CTT GGG GGC GCT CTG AGC CTG      292
      Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu
      75              80              85
      ACC TTC GTG CTG GGG CTG CTT TCT GGC TTT TTG GTC TGG AGA CGA TGC      340
      Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys
30      90              95              100
      CGC AGG AGA GAG AAG TTC ACC ACC CCC ATA GAG GAG ACC GGC GGA GAG      388
      Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu
      105              110              115              120
      GGC TGC CCA GCT GTG GCG CTG ATC CAG TGACA ATGT GCCCCCTGCC A CCGG      440
35  Gly Cys Pro Ala Val Ala Leu Ile Gln
      125
      GGCTCGCCCA CTCATCATTC ATTCATCCAT TCTAGAGCCA GTCTCTGCCT CCCAGACGCG      500
      GCGGGAGCCA AGCTCCTCCA ACCACAAGGG GGGTGGGGGG CGGTGAATCA CCTCTGAGGC      560

```

CTGGGCCCAG GGTTCAGGGG AACCTTCCAA GGTGTCTGGT TGCCCTGCCT CTGGCTCCAG 620  
 AACAGAAAGG GAGCCTCACG CTGGCTCACA CAAAACAGCT GACACTGACT AAGGAACTGC 680  
 AGCATTGCA CAGGGGAGGG GGGTGCCCTC CTCCTAGAG GCCCTGGGGG CCAGGCTGAC 740  
 TTGGGGGGCA GACTTGACAC TAGGCCCCAC TCACTCAGAT GTCCTGAAAT TCCACCACGG 800  
 5 GGGTCACCT GGGGGGTTAG GGACCTATTT TTAACACTAG GGGGCTGGCC CACTAGGAGG 860  
 GCTGGCCCTA AGATACAGAC CCCCCCAACT CCCCAGCG GGGAGGAGAT ATTTATTTTG 920  
 GGGAGAGTTT GGAGGGGAGG GAGAATTTAT TAATAAAGA ATCTTTAACT TT 972

10 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 15 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- 20 (B) CELL KIND: Liver
- (C) CELL LINE:
- (D) CLONE NAME: HP10433

(ix) SEQUENCE CHARACTERISTICS:

- 25 (A) CHARACTERIZATION CODE: CDS
- (B) EXISTENCE POSITION: 73.. 564
- (C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

30 AAGATTTTCAG CTGCGGGACG GTCAGGGGAG ACCTCCAGGC GCAGGGAAGG ACGGCCAGGG 60  
 TGACACGGAA GC ATG CGA CGG CTG CTG ATC CCT CTG GCC CTG TGG CTG GGC 111  
 Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly  
 1 5 10  
 35 GCG GTG GGC GTG GGC GTC GCC GAG CTC ACG GAA GCC CAG CGC CGG GGC 159  
 Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly  
 15 20 25  
 CTG CAG GTG GCC CTG GAG GAA TTT CAC AAG CAC CCG CCC GTG CAG TGG 207

	Leu	Gln	Val	Ala	Leu	Glu	Glu	Phe	His	Lys	His	Pro	Pro	Val	Gln	Trp	
	30				35						40					45	
	GCC	TTC	CAG	GAG	ACC	AGT	GTG	GAG	AGC	GCC	GTG	GAC	ACG	CCC	TTC	CCA	255
	Ala	Phe	Gln	Glu	Thr	Ser	Val	Glu	Ser	Ala	Val	Asp	Thr	Pro	Phe	Pro	
5					50					55					60		
	GCT	GGA	ATA	TTT	GTG	AGG	CTG	GAA	TTT	AAG	CTG	CAG	CAG	ACA	AGC	TGC	303
	Ala	Gly	Ile	Phe	Val	Arg	Leu	Glu	Phe	Lys	Leu	Gln	Gln	Thr	Ser	Cys	
					65					70					75		
	CGG	AAG	AGG	GAC	TGG	AAG	AAA	CCC	GAG	TGC	AAA	GTC	AGG	CCC	AAT	GGG	351
10	Arg	Lys	Arg	Asp	Trp	Lys	Lys	Pro	Glu	Cys	Lys	Val	Arg	Pro	Asn	Gly	
		80						85					90				
	AGG	AAA	CGG	AAA	TGC	CTG	GCC	TGC	ATC	AAA	CTG	GGC	TCT	GAG	GAC	AAA	399
	Arg	Lys	Arg	Lys	Cys	Leu	Ala	Cys	Ile	Lys	Leu	Gly	Ser	Glu	Asp	Lys	
		95					100					105					
15	GTT	CTG	GGC	CGG	TTG	GTC	CAC	TGC	CCC	ATA	GAG	ACC	CAA	GTT	CTG	CGG	447
	Val	Leu	Gly	Arg	Leu	Val	His	Cys	Pro	Ile	Glu	Thr	Gln	Val	Leu	Arg	
		110				115					120				125		
	GAG	GCT	GAG	GAG	CAC	CAG	GAG	ACC	CAG	TGC	CTC	AGG	GTG	CAG	CGG	GCT	495
	Glu	Ala	Glu	Glu	His	Gln	Glu	Thr	Gln	Cys	Leu	Arg	Val	Gln	Arg	Ala	
20					130					135					140		
	GGT	GAG	GAC	CCC	CAC	AGC	TTC	TAC	TTC	CCT	GGA	CAG	TTC	GCC	TTC	TCC	543
	Gly	Glu	Asp	Pro	His	Ser	Phe	Tyr	Phe	Pro	Gly	Gln	Phe	Ala	Phe	Ser	
					145					150					155		
	AAG	GCC	CTG	CCC	CGC	AGC	TAAGCCAGCA	CTGAGCTGCG	TGGTGCCTC								590
25	Lys	Ala	Leu	Pro	Arg	Ser											
					160												
	CAGGACCGCT	GCCGGTGGTA	ACCACTGGAA	GACCCAGCC	CCCAGGGAGA	GGACCCCGTT											650
	CTATCCCCAG	CCATGATAAT	AAAGCTGCTC	TCCCAGCTGC	CTCTC												695

30

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1914

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA



## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10480

5

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 80.. 661  
 (C) CHARACTERIZATION METHOD: E

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

	ACTCTCTGCT GTCGCCCCGTC CCGCGCGCTC CTCCGACCCG CTCCGCTCCG CTCCGCTCGG	60
	CCCCGCGCCG CCCGTCAAC ATG ATC CGC TGC GGC CTG GCC TGC GAG CGC TGC	112
15	Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys	
	1 5 10	
	CGC TGG ATC CTG CCC CTG CTC CTA CTC AGC GCC ATC GCC TTC GAC ATC	160
	Arg Trp Ile Leu Pro Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile	
	15 20 25	
20	ATC GCG CTG GCC GGC CGC GGC TGG TTG CAG TCT AGC GAC CAC GGC CAG	208
	Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln	
	30 35 40	
	ACG TCC TCG CTG TGG TGG AAA TGC TCC CAA GAG GGC GGC GGC AGC GGG	256
	Thr Ser Ser Leu Trp Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly	
25	45 50 55	
	TCC TAC GAG GAG GGC TGT CAG AGC CTC ATG GAG TAC GCG TGG GGT AGA	304
	Ser Tyr Glu Glu Gly Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg	
	60 65 70 75	
	GCA GCG GCT GCC ATG CTC TTC TGT GGC TTC ATC ATC CTG GTG ATC TGT	352
30	Ala Ala Ala Ala Met Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys	
	80 85 90	
	TTC ATC CTC TCC TTC TTC GCC CTC TGT GGA CCC CAG ATG CTT GTC TTC	400
	Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe	
	95 100 105	
35	CTG AGA GTG ATT GGA GGT CTC CTT GCC TTG GCT GCT GTG TTC CAG ATC	448
	Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile	
	110 115 120	
	ATC TCC CTG GTA ATT TAC CCC GTG AAG TAC ACC CAG ACC TTC ACC CTT	496

